

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2004, 03:13:58 ; Search time 8782.76 Seconds
(without alignments)
10940.929 Million cell updates/sec

Title: US-09-894-749-1
Perfect score: 2217
Sequence: 1 gaattcggttcattctaa.....aaaaaaaaagggcgccgc 2217

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
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- 3: gb.in.*
- 4: gb.on.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
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- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.ro.*
- 21: em.sts.*
- 22: em.ov.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	2217	100.0	2217	6	AR214935	Sequence
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5	2064.4	93.1	2136	9	AK057114	Homo sapi
6	2063.2	93.1	2164	9	BC020632	Homo sapi
7	2041.6	92.1	2144	6	AX299976	Sequence
8	2041.6	92.1	2144	9	AF268036	Homo sapi
9	1753.2	79.1	1840	6	AX299975	Sequence
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45	152.4	6.9	1458	10	BC061969	Rattus no

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Sequence 1 from patent US 6274362.
ACCESSION AR165090
VERSION AR165090.1
KEYWORDS GI:16238486
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2217)
AUTHORS Hodge,M.R. and Yowe,D.
TITLE RGS-containing molecules and uses thereof
JOURNAL Patent: US 6274362-A 1 14-AUG-2001;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a


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RESULT 4
AF076642 2138 bp mRNA linear PRI 01-JUL-2000
LOCUS Homo sapiens regulator of G-protein signaling 13 mRNA, complete
DEFINITION
ACCESSION AF076642
VERSION AF076642.1 GI:8985627
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2138)
AUTHORS Zhang, W., Wan, T., Yuan, Z., He, L. and Cao, X.
TITLE A novel regulator of G-protein signaling
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2138)
AUTHORS Zhang, W., Wan, T., Yuan, Z., He, L. and Cao, X.
TITLE Direct Submission
JOURNAL Submitted (07-JUL-1998) Department of Immunology, Shanghai
Brilliance Biotechnology Institute & Second Military Medical
University, 800 Xiangyin Road, Shanghai 200433, P.R. China
FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 0;
Matches 2068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 412 GACAAACTCTTTCCCATAGAGATGAGCTAGAGGCTTTTACCAGATTTCTTAAACTGAA 471
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RESULT 5.

AK057114 2136 bp mRNA linear PRI 01-AUG-2002
LOCUS AK057114
DEFINITION Homo sapiens cDNA FLJ32552 fis, clone SPLEN100089, highly similar to Homo sapiens regulator of G-protein signaling 13 mRNA.

ACCESSION AK057114.1 GI:16552701

VERSION AK057114.1

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R.,

Osuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J.,

Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K.,

Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H.,

Kanda, K., Watanabe, M., Murakawa, K., Kanehori, K.,

Takanashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahara, K.,

Masuko, Y., Nagai, K., and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 2136)

Isogai, T., Otsuki, T., and Sugiyama, T.

Direct Submission

JOURNAL

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

FEATURES

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Source

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 VERSION BC020632.1 GI:18089322
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bukaryova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2164)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
 Schetzl,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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 Bouford,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
 Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butlerfield,Y.S., Krzyzanski,M.I., Skalska,U., Smalish,D.E.,
 Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 12477932
 2 (bases 1 to 2164)
 Strausberg,R.
 Direct Submission
 Submitted (03-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-r@mail.nih.gov
 Tissue procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.W.A.G.E. Consortium (LINL)
 DNA Sequencing by: Sequencing Group at the Stanford Human
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) mcdpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.W.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: IRAL Plate: 37 Row: d Column: 18
 This clone was selected for full length sequencing because it
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ACCESSION	AX299976			
VERSION	AX299976.1	GI:17129463		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	Murray,D.L. and Gagnon,A.W.			
TITLE	Nucleic acids encoding a novel regulator of G protein signaling, rgs18, and uses thereof			
JOURNAL	Patent: WO 0183514-A 19 08-NOV-2001;			
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2144)
Gagnon,A.W., Murray,D.L. and Leadley,R.J. Jr.
Cloning and characterization of a novel regulator of G protein
signalling in human platelets
Cell. Signal. 14 (7), 595-606 (2002)
21952499
MEDLINE
PUBMED
11955952
REFERENCE
2 (bases 1 to 2144)
Gagnon,A.W., Murray,D.L. and Leadley,R.J. Jr.
Direct Submission
Submitted (16-MAY-2000) Pfizer Central Research, Eastern Point Rd,
Groton, CT 06340, USA
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Best Local Similarity 99.5%; Pred. No. 0;
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VERSION	AX299975.1	GI:17129462	
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ORGANISM	Homo sapiens		
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AUTHORS	Murray, D.L. and Gagnon, A.W.		
TITLE	Nucleic acids encoding a novel regulator of G protein signaling, rgs18, and uses thereof		
JOURNAL	Patent: WO 0183514-A 18 08-NOV-2001; Aventis Pharmaceuticals Products Inc. (US)		
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Qy	121	GATGTAATAAATAGACATCTCTCAATTTTACAGAGAGATGGAACCAACATGCTGTTTC	180
Db	124	GATGTAATAAATAGACATCTCTCAATTTTACAGAGAGATGGAACCAACATGCTGTTTC	183
Qy	181	TTTTTCTCAATAAATATGTGTAATCAAAAGAAAAAATTTTTTCAAGTTAATACATGGT	240
Db	184	TTTTTCTCAATAAATATGTGTAATCAAAAGAAAAAATTTTTTCAAGTTAATACATGGT	243
Qy	241	TCAGGAAAGAGAAACACAGCAAGAGCCAAATCAGACTTAAGGAAAGAAATAGA	300

Db	244	TCAGGAAAGAGAAACACAGCAAGCCAAATTCAGAGCTTAAGGAAAGAAATAGA	303
Qy	301	CTAAGTCTCTTCTGTGAGAGAACTGAGTTTCATGAAGACACCCGCTCCAGTAGATCTGGG	360
Db	304	CTAAGTCTCTTCTGTGAGAGAACTGAGTTTCATGAAGACACCCGCTCCAGTAGATCTGGG	363
Qy	361	CACCTGGCCAAAGAAACAAAGAGTCTCCCTGAAGAGGAGTGAATGGGGTGAATCATTT	420
Db	364	CACCTGGCCAAAGAAACAAAGAGTCTCCCTGAAGAGGAGTGAATGGGGTGAATCATTT	423
Qy	421	GACAAATCTGTTTCCCATAGAGTGCATAGAGGCTTTTACAGATTTCTTAAAACTGAA	480
Db	424	GACAAATCTGTTTCCCATAGAGTGCATAGAGGCTTTTACAGATTTCTTAAAACTGAA	483
Qy	481	TTCAAGTGAAGAAATATTTGAATTTTGGATAGCTCTGTAAGATTTCAAGAAAGCAAGGGA	540
Db	484	TTCAAGTGAAGAAATATTTGAATTTTGGATAGCTCTGTAAGATTTCAAGAAAGCAAGGGA	543
Qy	541	CCTCAACAAATTCACCTTAAAGCAAGCAATATATGCAATTTTATACAGACTGATGCC	600
Db	544	CCTCAACAAATTCACCTTAAAGCAAGCAATATATGCAATTTTATACAGACTGATGCC	603
Qy	601	CCAAAAGAGTTAACTTCAACAAAGAAAGTCAATTTACAAAACAGCATCACTCAA	660
Db	604	CCAAAAGAGTTAACTTCAACAAAGAAAGTCAATTTACAAAACAGCATCACTCAA	663
Qy	661	CCTACCTCCACAGTTTGTGCTGCAAGAGAGTGTATCAGCTCATGGAACAGAC	720
Db	664	CCTACCTCCACAGTTTGTGCTGCAAGAGAGTGTATCAGCTCATGGAACAGAC	723
Qy	721	AGTTATACAGTTTCTGAAATCTGACATCTTTTAGACTTGTATGGAAGAGAGACTCAG	780
Db	724	AGTTATACAGTTTCTGAAATCTGACATCTTTTAGACTTGTATGGAAGAGAGACTCAG	783
Qy	781	AGACCAACAAATCTTAGGAGACGATCACCTCATTTACCTGCAATGAATTCAGAGTGA	840
Db	784	AGACCAACAAATCTTAGGAGACGATCACCTCATTTACCTGCAATGAATTCAGAGTGA	843
Qy	841	CAATCAGATGTTGCCATTTGTTTAAAGAAATGATTTTCTCATTTTATGACAAAC	900
Db	844	CAATCAGATGTTGCCATTTGTTTAAAGAAATGATTTTCTCATTTTATGACAAAC	903
Qy	901	TTATACATCTGCTTCTTAAACATATCGATGTTTATGTAAGATTTGTCCTCCCTTTAA	960
Db	904	TTATACATCTGCTTCTTAAACATATCGATGTTTATGTAAGATTTGTCCTCCCTTTAA	963
Qy	961	CTGAATATGTCATGTAATTTTAAAGTAAAGCAACAACTTCTGCTACAAA	1020
Db	964	CTGAATATGTCATGTAATTTTAAAGTAAAGCAACAACTTCTGCTACAAA	1023
Qy	1021	ATACATACAGTATCTGCCAGTATATCTGTAAACCTCTTATTTGATGTCAATTCATTTA	1080
Db	1024	ATACATACAGTATCTGCCAGTATATCTGTAAACCTCTTATTTGATGTCAATTCATTTA	1083
Qy	1081	TAATCAGAAAAAAACCTTATTTCTTAATCAAGGAGTACAAAAAGTAAATATGTTT	1140
Db	1084	TAATCAGAAAAAAACCTTATTTCTTAATCAAGGAGTACAAAAAGTAAATATGTTT	1143
Qy	1141	TATAAGATTTGATGATTAAGTAAAGTAAAGCTTTTGCAGAAAGTGTCAAAAGTCAACA	1200
Db	1144	TATAAGATTTGATGATTAAGTAAAGTAAAGCTTTTGCAGAAAGTGTCAAAAGTCAACA	1203
Qy	1201	AAAGTCTAGTTGGATTTTACAAAGAGCAATATATGTTTATATAAACAATATAT	1260
Db	1204	AAAGTCTAGTTGGATTTTACAAAGAGCAATATATGTTTATATAAACAATATAT	1263
Qy	1261	ACTCAGATATCCAAATGTTTCAGATAGCATTTTTCATAATGAATGTCTCTTTTTTGGT	1320
Db	1264	ACTCAGATATCCAAATGTTTCAGATAGCATTTTTCATAATGAATGTCTCTTTTTTGGT	1323
Qy	1321	AATAGTGTAGAGTGTCTGTTCTTCAATGGAGATGAAGAACATTTATTTATTCGGTT	1380
Db	1324	AATAGTGTAGAGTGTCTGTTCTTCAATGGAGATGAAGAACATTTATTTATTCGGTT	1383

QY 1381 ACTACTAACCTGTCCCAAGATAGTAAATATACACCTCTAGTTATTAAGCCAGCAACAGGAA 1440
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 QY 1441 CTTTGTGAAGACACATTCATCTCTACAGAACTTCAGATTAAATATATATCTAGATTAAATG 1500
 Db 1444 CTTTGTGAAGACACATTCATCTCTACAGAACTTCAGATTAAATATATATCTAGATTAAATG 1503
 QY 1501 ACTGAGATAGATCCCATTTGAATCTATTCCTTAAGTGAACATGGAGGATACCCAGTTAT 1560
 Db 1504 ACTGAGATAGATCCCATTTGAATCTATTCCTTAAGTGAACATGGAGGATACCCAGTTAT 1563
 QY 1561 ACAAAAGTACTTCTGTGTGTACAGAAACATGACAGATTTTGCATATCTCCAGCTAGGGA 1620
 Db 1564 ACAAAAGTACTTCTGTGTGTACAGAAACATGACAGATTTTGCATATCTCCAGCTAGGGA 1623
 QY 1621 ACTAAGTATAGATCTTATTCACCGCTAAGAAACTTCTACTACTAACTATTAGGCCATCA 1680
 Db 1624 ACTAAGTATAGATCTTATTCACCGCTAAGAAACTTCTACTACTAACTATTAGGCCATCA 1683
 QY 1681 ATGGCTTGAATATAAAACAGAGAGGTTTTTCCAGGACGCTCTCATGTTTGGCCCTTTAG 1740
 Db 1684 ATGGCTTGAATATAAAACAGAGAG-GTTTTTCCAGGACGCTCTCATGTTTGGCCCTTTAG 1742
 QY 1741 AATGGGTGAGAAATCAGAAATGAGATGAGGGGAGAGCAAGGAGTCTAAGGCCCTAGC 1800
 Db 1743 AATGGGTGAGAAATCAGAAATGAGATGAGGGGAGAGCAAGGAGTCTAAGGCCCTAGC 1802
 QY 1801 GATTTGGGCATCTGCCATTTGGTTTCATATTTCAGAAAG 1838
 Db 1803 GATTTGGGCATCTGCCATTTGGTTTCATATTTCAGAAAG 1840

RESULT 10
 LOCUS AL513175 94175 bp DNA linear PRI 15-NOV-2001
 DEFINITION Human DNA sequence from clone RP11-142L4 on chromosome 1, complete sequence.

ACCESSION AL513175
 VERSION AL513175.10 GI:16973028
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Martin,S.
 Direct Submission
 Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 On Nov 16, 2001 this sequence version replaced gi:15620649.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping

Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl>
 RP11-142L4 is from the library RP11-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACe3.6
 IMPORTANT: This sequence is not the entire insert of clone RP11-142L4. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-142L4 is at 94175 in this sequence. The true left end of clone RP11-513B7 is at 2955 in this sequence. The true right end of clone RP11-198A7 is at 2000 in this sequence.

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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosomes="1"
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 /notes="Sequence from overlapping clones RP11-513 (ALJ57566) and RP1-314M19 (ALJ91274). Assembly confirmed by restriction digest."
 misc_feature 41580
 /notes="Tandem repeat. Forced join. Gap size estimated to be approximately 50bp by restriction digest data."

ORIGIN

Query Match 71.3%; Score 1581; DB 9; Length 94175;
 Best Local Similarity 99.1%; Pred. No. 4,9e-248;
 Matches 1590; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 608 AGGTAAACCTTGATTTTTCACAAAAAGAGTCAATTACAAACAGCATCACTCAACCTACCC 667
 Db 2737 AGGTAAACCTTGATTTTTCACAAAAAGAGTCAATTACAAACAGCATCACTCAACCTACCC 2796
 QY 668 TCACAGTTTTGATGTCGACAAAGCAGAGTGTATCAGTCTATGGAACAGACAGTTATA 727
 Db 2797 TCACAGTTTTGATGTCGACAAAGCAGAGTGTATCAGTCTATGGAACAGACAGTTATA 2856
 QY 728 CAGTTTTCTGAATCTGCATCTATTAGACTTTGATGGAAGGAAGACCTCAGAGACCAA 787
 Db 2857 CAGTTTTCTGAATCTGCATCTATTAGACTTTGATGGAAGGAAGACCTCAGAGACCAA 2916
 QY 788 CAAATCTTAGGAGACGATCAGCTCATTTACCTGCAATGAATCCAAAGATGTCAATCAG 847
 Db 2917 CAAATCTTAGGAGACGATCAGCTCATTTACCTGCAATGAATCCAAAGATGTCAATCAG 2976
 QY 848 ATGTTGCCATTGGTTATTAAGAAATTCATTTTGCTCATTTTATGACAACTTATACA 907
 Db 2977 ATGTTGCCATTGGTTATTAAGAAATTCATTTTGCTCATTTTATGACAACTTATACA 3036
 QY 908 TCTGCTTCTAACATATCGCATGTTTATGTTAAGATTGGTCCCATCTTTAAACTGAAT 967
 Db 3037 TCTGCTTCTAACATATCGCATGTTTATGTTAAGATTGGTCCCATCTTTAAACTGAAT 3096
 QY 968 ATGTCATGCAATATTTTAAATAATGTAATAACAAACAACTTCTGCTACAAATAACATA 1027
 Db 3097 ATGTCATGCAATATTTTAAATAATGTAATAACAAACAACTTCTGCTACAAATAACATA 3156
 QY 1028 CAGTATCTGCAGTATATCTGTAAACCTTCTATTGATGTCATTCCTATTAATATCAG 1087
 Db 3157 CAGTATCTGCAGTATATCTGTAAACCTTCTATTGATGTCATTCCTATTAATATCAG 3216
 QY 1088 AAAAAAACTATTTCTTAATCAAAAGGAGTACAAAAAGGATTAATGTTTTATAGA 1147
 Db 3217 AAAAAAACTATTTCTTAATCAAAAGGAGTACAAAAAGGATTAATGTTTTATAGA 3276
 QY 1148 TTCTAGATTAGTAAAGTTAGCTTTTGCAGAGTTGTCAAAGTGTCAAAGTGTCAAAGAGTCT 1207
 Db 3277 TTCTAGATTAGTAAAGTTAGCTTTTGCAGAGTTGTCAAAGTGTCAAAGTGTCAAAGAGTCT 3336

Homo sapiens chromosome 1 clone RP1-314M19 map q31.1-31.3, 14
unordered pieces.
AL391274
AL391274.4 GI:9931017
HTG; HTGS_PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
McLay, K.
Direct Submission
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humqurysanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced qi:9926780.

	DEFINITION
QY	1208 AGTTGGGATTTTTTACCBAAGCAGCATAATATGTGTATATAAACATAATAATACTACTAGA 1267
DB	3337 AGTTGGGATTTTTTACCBAAGCAGCATAATATGTGTATATAAACATAATAATACTACTAGA 3396
QY	1268 TATCCAAATGTTTCAGATAGCATTTCATATATGAATGTTCTCTTTTTTTTGGTAATAGTG 1327
DB	3397 TATCCAAATGTTTCAGATAGCATTTCATATATGAATGTTCTCTTTTTTTTGGTAATAGTG 3456
QY	1328 TAGAAGTGATCTGGTTCCTTACAATGGGAGATGAAGACATTATTATTTGGGTTACTACTA 1387
DB	3457 TAGAAGTGATCTGGTTCCTTACAATGGGAGATGAAGACATTATTATTTGGGTTACTACTA 3516
QY	1388 ACCCTGTCCCAAGAATAAGTAAATATCACTCTAGTTTATAAGCCAGCAACAGGAACTTTTGT 1447
DB	3517 ACCCTGTCCCAAGAATAAGTAAATATCACTCTAGTTTATAAGCCAGCAACAGGAACTTTTGT 3576

FEATURES

RESULT 11				
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LOCUS	AL391274	107919 bp	DNA	linear
				HTG 11-SEP-2001

Db 44249 TTTTCTCTTTAGAGTAATATTGGGATAGAAAGTATTAAATTGAG 44293

RESULT 12
AX299963
LOCUS AX299963 1486 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 6 from Patent WO0183514.
ACCESSION AX299963
VERSION AX299963.1 GI:17129454
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Murray,D.L. and Gagnon,A.W.
TITLE Nucleic acids encoding a novel regulator of G protein signaling,
rgs19, and uses thereof
JOURNAL Patent: WO 0183514-A 6 08-NOV-2001;
Aventis Pharmaceuticals Products Inc. (US)
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/db_xref="taxon:9606"
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Best Local Similarity 99.4%; Pred. No. 4.7e-226;
Matches 1464; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
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Db 1 CTCACCTTACCTCCACAGTTTGTGTCGACAAAGCAGAGTGTATCAGCTCATGGAAC 60
QY 716 AAGACAGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTGTAGGAAGAAC 775
Db 61 AAGACAGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTGTAGGAAGAAC 120
QY 776 CTCAGAGCAACAATCTTAGAGACGATCAGCTCATTTACCTGCAATGAATCCAG 835
Db 121 CTCAGAGCAACAATCTTAGAGACGATCAGCTCATTTACCTGCAATGAATCCAG 180
QY 836 ATGTACAATCAGATGTGCAATTTGTTTATGAAGAAATTTGATTTGCTCATTTTATGA 895
Db 181 AITGCAATCAGATGTGCAATTTGTTTATGAAGAAATTTGATTTGCTCATTTTATGA 240
QY 896 CAACTTATACATCTGCTTCTAACATATCGCATGTTTATGTTAAGATTTGCTCCCATCT 955
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Db 421 ATTATATCAGAAAAAATCTTTCTTATCAAGGAGTACAAAAAGTAAATA 480
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Db 481 TGTATTAAGATTTGTAGAGTTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 540
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Db 601 ATAATCTCAGATATCCAAATGTTTCAGATAGATTTTTCATTAAGATGTTCTCTTTT 660
QY 1316 TTGGTAATAGTGTAGAAGTGATCTGGTTCTTAACAATGGAGATGAAGAACATTTATTATT 1375
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Db 781 AGGAACCTTTTGTGAAGACACATTCATCTCTACAGAACTTCAGATTAAATATAATCTAGAT 840
QY 1496 TAATGCTGAGAAATAGATCCACATTTGAACTCATCTTAAGTGAACATGGAGCTACCCA 1555
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QY 1556 GTTATACAAAGTACTTCTGTTGTCACAGAAACATGACAGATTTTGCAATATCTCCAGGT 1615
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QY 1616 AGGAACTAAGTAGACTCTTATCACCGCTTAAGAAACCTTGCTACTAACTATTAGGC 1675
Db 961 AGGAACTAAGTAGACTCTTATCACCGCTTAAGAAACCTTGCTACTAACTATTAGGC 1020
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QY 1856 TATTCCTGTTTAAAGCAATCTCCTTAAAGTAAATTTATTTCAAAATAAGATTATCTCATCA 1915
Db 1200 TATTCCTGTTTAAAGCAATCTCCTTAAAGTAAATTTATTTCAAAATAAGATTATCTCATCA 1259
QY 1916 TCTATATGTCATGTTTAAAGAGATATTTAATTTAATGTTGTTGTTAGCTGCTGTA 1975
Db 1260 TCTATATGTCATGTTTAAAGAGATATTTAATTTAATGTTGTTGTTAGCTGCTGTA 1319
QY 1976 ATATTTGTTTAAAGCAATCTCCTTAAAGTAAATTTATTTCAAAATAAGATTATCTCATCA 2035
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QY 2036 AAAATGTGAACCTTTAGATCAATTTGATGTAATAATAATTTTAACTTCAATTCATCACT 2095
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RESULT 13
AR165091
LOCUS AR165091 1164 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6274362.
ACCESSION AR165091
VERSION AR165091.1 GI:16238488
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1164)
AUTHORS Hodge,M.R. and Yowe,D.
TITLE RGS-containing molecules and uses thereof

[illegible]

Search completed: August 20, 2004, 09:58:55
Job time : 8791.76 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2004, 01:52:23 ; Search time 919.324 seconds
(without alignments)
10244.763 Million cell updates/sec

Title: US-09-894-749-1

Perfect score: 2217

Sequence: 1 gaattggcttccatcctaa.....aaaaaaaaagggcgccgc 2217

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2041.6	92.1	2144	6	AA518340 Full leng
4	1816	81.9	1884	6	ABQ99387 Human cod
5	1753.2	79.1	1840	6	AA518339 5'-RACE C
6	1448.2	65.3	1486	6	AA518331 cDNA from
7	782	35.3	848	6	ABQ98617 Human ORF
8	596	26.9	1164	3	AA52090 Murine RG
9	596	26.9	1164	6	AA52090 Murine re
10	227.2	10.2	241	6	AA518334 cDNA enco
11	158.4	7.1	408	4	AAH76414 RGS prote
12	158.4	7.1	1795	4	AAH76414 RGS prote
13	155.6	7.0	1345	6	ABT10881 Human bre
14	155.6	7.0	1345	6	ABX83834 Human cDN
15	155.6	7.0	1345	7	ACC46750 Human COP
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18	155.6	7.0	1364	3	AA516132 Human pro
19	155.6	7.0	1362	9	ADB47313 Human cDN
20	153.2	6.9	745	2	AAV38084 Human reg
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22	153.2	6.9	1923	3	AA51745 DNA enco
23	153.2	6.9	1923	6	ABQ92597 Human sec

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25	152.4	6.9	1629	7	ABT42293 Toxicity
26	145.2	6.5	543	6	ABL99975 Rat disea
27	145.2	6.5	817	6	ABL99979 Rat disea
28	143.8	6.5	800	7	ACA56493 Human sig
29	143.8	6.5	1238	4	AA126766 Human bre
30	143.8	6.5	2934	6	ABK47336 cDNA enco
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35	141.2	6.4	1227	7	ABX74448 Human cDN
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38	141.2	6.4	1398	5	AAF68404 Human lun
39	141.2	6.4	1398	6	ABK38315 cDNA enco
40	141.2	6.4	1398	6	ABK64672 Human ben
41	141.2	6.4	1398	7	ACC46754 Human COP
42	141.2	6.4	1398	7	ACA56692 Signallin
43	141.2	6.4	1398	7	ACA10644 Human lun
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ALIGNMENTS

RESULT 1
AAA52089
ID AAA52089 standard; cDNA; 2217 BP.
XX AC AAA52089;
XX DT 04-DEC-2000 (first entry)
XX DE Human RGS protein coding sequence.
XX KW RGS; regulators of G-protein signaling; GTPase activating protein; GAP;
XX KW G-alpha protein; cell adhesion; chemotaxis; vulnery; immunosuppressor;
XX KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
XX KW cytosolic; hepatotropic; anti-anaemic; modulator; gene therapy; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 160..867
XX FT /*tag= a
XX FT /product= "RGS_protein"
XX PN WO200046236-A2.
XX PD 10-AUG-2000.
XX PF 04-FEB-2000; 2000WO-US002977.
XX PR 04-FEB-1999; 99US-00244314.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Hodge MR, Yowe D;
XX DR WPI; 2000-532893/48.
XX DR P-PSDB; AAY97153.
XX PT Novel regulator of G-protein signaling nucleic acids and polypeptides,
XX PT useful as diagnostic and investigative tools and to treat G-protein
XX PS Claim 1; Page 100-102; 105pp; English.
XX CC The RGS (regulators of G-protein signaling) protein genes, clones
XX CC AAH16395 and m1975, were identified in human and murine spleen cDNA
XX CC libraries, respectively. Both proteins have unique N- and C-terminal

CC sequences. The C-terminal location of the RGS domain is consistent with
 CC RGSs known to act as GTPase activating proteins (GAPs) for G-alpha
 CC proteins. G-alpha-1 linked receptors support rapid adhesion and directed
 CC migration of leukocytes and other cell types. The novel RGS proteins may
 CC be used to modulate cell adhesion and chemotaxis, e.g. for aiding wound
 CC repair. The RGS proteins, related cDNAs and anti-RGS antibodies are
 CC useful for modulation, diagnosis and treatment of immune and respiratory
 CC disorders

XX
 SQ Sequence 2217 BP; 801 A; 359 C; 380 G; 677 T; 0 U; 0 Other;

Query Match 100.0%; Score 2217; DB 3; Length 2217;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGCTTCCATCCTAATAGACTCACTATAGGCTCGAGCGGCCCGCGGCAGGT 60
 DB |||||
 QY 1 GAATTCGGCTTCCATCCTAATAGACTCACTATAGGCTCGAGCGGCCCGCGGCAGGT 60
 DB |||||

QY 61 ATAACTTTTATTTCTACTATGTATGTATGAATAGTATTAAATCAACTAGGGAAG 120
 DB |||||

QY 61 ATAACTTTTATTTCTACTATGTATGTATGAATAGTATTAAATGAATAGGGAAG 120
 DB |||||

QY 121 GATGTAATTAATTAGACATCTCTTCAATTTAGAGAGAGATGGAACAACATGCTTTTC 180
 DB |||||

QY 121 GATGTAATTAATTAGACATCTCTTCAATTTAGAGAGAGATGGAACAACATGCTTTTC 180
 DB |||||

QY 181 TTTTCTCAATAAATATGTGTGAATCAAAAGAAAAAATCTTTTCAAGTTAATCATCGT 240
 DB |||||

QY 181 TTTTCTCAATAAATATGTGTGAATCAAAAGAAAAAATCTTTTCAAGTTAATCATCGT 240
 DB |||||

QY 241 TCAGGAAAGAGAGAAACAAGCAAGAGCCAAATCAGAGCTAAGGAAAAAGAAATAGA 300
 DB |||||

QY 241 TCAGGAAAGAGAGAAACAAGCAAGAGCCAAATCAGAGCTAAGGAAAAAGAAATAGA 300
 DB |||||

QY 301 CTAAGTCCTTGTGAGAACTCAGTTTCATGAGACACCCGCTCCAGTAGATCTGGG 360
 DB |||||

QY 301 CTAAGTCCTTGTGAGAACTCAGTTTCATGAGACACCCGCTCCAGTAGATCTGGG 360
 DB |||||

QY 361 CACTTGGCCAAAGAAACAAGAGTCTCCCTGAGAGGCGAGTGAATGGGTAATCAIT 420
 DB |||||

QY 361 CACTTGGCCAAAGAAACAAGAGTCTCCCTGAGAGGCGAGTGAATGGGTAATCAIT 420
 DB |||||

QY 421 GACAACTCTTCCATAGAGATGAGCTAGAGGCTTTTACCAGATTTCTTAAACTGAA 480
 DB |||||

QY 421 GACAACTCTTCCATAGAGATGAGCTAGAGGCTTTTACCAGATTTCTTAAACTGAA 480
 DB |||||

QY 481 TTCAAGTGAAGAAAAATATTGAATTTTGGATAGCTCTGAAGATTTCAAGAAAAAGCAAGGGA 540
 DB |||||

QY 481 TTCAAGTGAAGAAAAATATTGAATTTTGGATAGCTCTGAAGATTTCAAGAAAAAGCAAGGGA 540
 DB |||||

QY 541 CTTCAACAAATTCACCTTAAAGCAAAAGCAATATATAGAAATTTATACAGACTGATGCC 600
 DB |||||

QY 541 CTTCAACAAATTCACCTTAAAGCAAAAGCAATATATAGAAATTTATACAGACTGATGCC 600
 DB |||||

QY 601 CCAAAAGAGTTTAACTTGAATTTTCAACAAGAAAGTCAATTTACAAACAGCATCACTCA 660
 DB |||||

QY 601 CCAAAAGAGTTTAACTTGAATTTTCAACAAGAAAGTCAATTTACAAACAGCATCACTCA 660
 DB |||||

QY 661 CTTACCCCTCCACAGTTTGTATGCTGCCAAAGCAGAGTGTATCAGCTCATGGAACAAGAC 720
 DB |||||

QY 661 CTTACCCCTCCACAGTTTGTATGCTGCCAAAGCAGAGTGTATCAGCTCATGGAACAAGAC 720
 DB |||||

QY 721 AGTTATACAGCTTTTCTGAAATCTGACATCTATTTAGACTTTGATGGAAGGAGACCTCAG 780
 DB |||||

QY 721 AGTTATACAGCTTTTCTGAAATCTGACATCTATTTAGACTTTGATGGAAGGAGACCTCAG 780
 DB |||||

QY 781 AGACCAACAAATCTTTAGGAGAGATCAGGCTCAITTTACCTGCAATGAATTTCAAGATGTA 840
 DB |||||

QY 781 AGACCAACAAATCTTTAGGAGAGATCAGGCTCAITTTACCTGCAATGAATTTCAAGATGTA 840
 DB |||||

QY 841 CAATCAGATGTGCGCATTTGGTTATTAAGAAAAATGTATTTGCTCAITTTTATGCAAAAC 900
 DB |||||

DB 841 CAATCAGATGTGCCATTTGGTTATTAAGAAAAATTCATTTTGTCTCATTTTATGACAAAC 900
 QY TTATACATCTGCTCTTAACATATCGGATGTTTATGTATAGATTTGGTCCCATCTTTAA 960
 DB TTATACATCTGCTCTTAACATATCGGATGTTTATGTATAGATTTGGTCCCATCTTTAA 960
 QY CTGAAATATGCTCATGTGAATTTATTTTAAAAATGTAAAAACAAACCTTTCTGTGTAACAA 1020
 DB CTGAAATATGCTCATGTGAATTTATTTTAAAAATGTAAAAACAAACCTTTCTGTGTAACAA 1020
 QY 1021 ATACATACATATCTGCCAGTATATTCGTGAAAAACCTTCTATTTGTATGTCATTTCCATTTA 1080
 DB 1021 ATACATACATATCTGCCAGTATATTCGTGAAAAACCTTCTATTTGTATGTCATTTCCATTTA 1080
 QY 1081 TAATCAGAAAAAATCTTATTTCTTAATCAAAAGGCGAGTACAAAAAAGTAATTAATGTTT 1140
 DB 1081 TAATCAGAAAAAATCTTATTTCTTAATCAAAAGGCGAGTACAAAAAAGTAATTAATGTTT 1140
 QY 1141 TATAAGATTGTAGAGTTAAAGTTAAAGCTTTTTCGAAAGTTGTCAAAAGTTCAAAACA 1200
 DB 1141 TATAAGATTGTAGAGTTAAAGTTAAAGCTTTTTCGAAAGTTGTCAAAAGTTGTCAAAACA 1200
 QY 1201 AAAGTCTAGTTGGGATTTTACCAAGCGAGCATATATGTGTTATATAAACAATAATAT 1260
 DB 1201 AAAGTCTAGTTGGGATTTTACCAAGCGAGCATATATGTGTTATATAAACAATAATAT 1260
 QY 1261 ACTCAGATATCCAAATGTTTCAGATAGCATTTTTCATAATGAATGTTCTCTTTTGTGTT 1320
 DB 1261 ACTCAGATATCCAAATGTTTCAGATAGCATTTTTCATAATGAATGTTCTCTTTTGTGTT 1320
 QY 1321 AATAGTGTAGAGTGTATCTGGTTCTTAATGAGGAGATGAAGAACATTTATTTATTTGGGTT 1380
 DB 1321 AATAGTGTAGAGTGTATCTGGTTCTTAATGAGGAGATGAAGAACATTTATTTATTTGGGTT 1380
 QY 1381 ACTACTAAACCTGTCCCAAGATAGTAATATCACCTCTAGTTTATAGCCAGCAACAGGAA 1440
 DB 1381 ACTACTAAACCTGTCCCAAGATAGTAATATCACCTCTAGTTTATAGCCAGCAACAGGAA 1440
 QY 1441 CTTTGTGAAAGACACATTCATCTCTACAGAACTTCAGATTTAAATATAATCTAGATTAATG 1500
 DB 1441 CTTTGTGAAAGACACATTCATCTCTACAGAACTTCAGATTTAAATATAATCTAGATTAATG 1500
 QY 1501 ACTGGAATATAGATCCACATTTTGAATCTCTCTAGTGAACATGAGACCTTACCCAGTTAT 1560
 DB 1501 ACTGGAATATAGATCCACATTTTGAATCTCTCTAGTGAACATGAGACCTTACCCAGTTAT 1560
 QY 1561 ACAAGTACTTCTGTTGGTCACAGAAACATGACAGATTTTGCATATCTCCAGGTAGGGA 1620
 DB 1561 ACAAGTACTTCTGTTGGTCACAGAAACATGACAGATTTTGCATATCTCCAGGTAGGGA 1620
 QY 1621 ACTAAGTAGACTTATATCAACGGCTAAGAAAACTTGTCTACTTAACTATTAGGCCATCA 1680
 DB 1621 ACTAAGTAGACTTATATCAACGGCTAAGAAAACTTGTCTACTTAACTATTAGGCCATCA 1680
 QY 1681 ATGGCTTGAATAAAAACACAGAGAGGTTTTCACAGAGCTCTCATGTTTGGCCCTTTAG 1740
 DB 1681 ATGGCTTGAATAAAAACACAGAGAGGTTTTCACAGAGCTCTCATGTTTGGCCCTTTAG 1740
 QY 1741 AATGGGGTAGAAATCAGAAATGAGATGAGGGGAAGCAAGGAGTCTAAGGCCCTAGC 1800
 DB 1741 AATGGGGTAGAAATCAGAAATGAGATGAGGGGAAGCAAGGAGTCTAAGGCCCTAGC 1800
 QY 1801 GATTTGGGATCTGCCACATTTGGTTTATTTTCAAGAAAGTGTATCTCATTTGATTTATTC 1860
 DB 1801 GATTTGGGATCTGCCACATTTGGTTTATTTTCAAGAAAGTGTATCTCATTTGATTTATTC 1860
 QY 1861 TTGTTAAGCAATCTCCTTAAAGTAATTTATTTCAAAATGAATTTACTCATACATCTAT 1920
 DB 1861 TTGTTAAGCAATCTCCTTAAAGTAATTTATTTCAAAATGAATTTACTCATACATCTAT 1920
 QY 1921 ATGTCACTGTTTAAAGAGATATTTAAATTTTAAATGTTGTTTACATGGTCTCTTAATAT 1980
 DB 1921 ATGTCACTGTTTAAAGAGATATTTAAATTTTAAATGTTGTTTACATGGTCTCTTAATAT 1980

481 TTCAGTGAAGAAAATATTGGAATTTTGGATAGCCTGTGAAGATTTCAAGAAAAGCAAGGGA 540
484 TTCAGTGAAGAAAATATTGGAATTTTGGATAGCCTGTGAAGATTTCAAGAAAAGCAAGGGA 543
541 CTTCAACAAATTCACCTTAAAGCAAAAGCAATATATAGAAATTTATACAGACTGATGCC 600
544 CTTCAACAAATTCACCTTAAAGCAAAAGCAATATATAGAAATTTATACAGACTGATGCC 603
601 CCAAGAGAGTTAACTCTGATTTTCAACAAAGAAAGTCAATPACAAAGCAATCACTCAA 660
604 CCAAGAGAGTTAACTCTGATTTTCAACAAAGAAAGTCAATPACAAAGCAATCACTCAA 663
661 CTTACCTCCACAGTTTGTATGCTGCACAAAGCAGAGTATACGCTCATGGACAAAGAC 720
664 CTTACCTCCACAGTTTGTATGCTGCACAAAGCAGAGTATACGCTCATGGACAAAGAC 723
721 AGTTATACAGTTTCTGAAATCTGACATCTATTTAGACTTATGATGGAAGGAAGCCTCAG 780
724 AGTTATACAGTTTCTGAAATCTGACATCTATTTAGACTTATGATGGAAGGAAGCCTCAG 783
781 AGACCAACAAATCTTAGGAGAGATCAGCTCATTTTACCTGCAATGAAATCCAGATGTA 840
784 AGACCAACAAATCTTAGGAGAGATCAGCTCATTTTACCTGCAATGAAATCCAGATGTA 843
841 CAATCAGATGTTGCCATTTGGTTATAAAGAAATTCATTTTGTCTCATTTTATGACAAAC 900
844 CAATCAGATGTTGCCATTTGGTTATAAAGAAATTCATTTTGTCTCATTTTATGACAAAC 903
901 TTATACATCTGTTCTTAACATATCGGATGTTATGTTAAGATTTGGTCCCATCTTTTAA 960
904 TTATACATCTGTTCTTAACATATCGGATGTTATGTTAAGATTTGGTCCCATCTTTTAA 963
961 CTGAAATATGTCATGTGAATTTATTTAAATGTTAAAGCAAACTTTCTGCTAACAAA 1020
964 CTGAAATATGTCATGTGAATTTATTTAAATGTTAAAGCAAACTTTCTGCTAACAAA 1023
1021 ATACATACAGTATCTGCCAGTATATCTGTAAACCTTCTATTTGATGTCATCTCAATTA 1080
1024 ATACATACAGTATCTGCCAGTATATCTGTAAACCTTCTATTTGATGTCATCTCAATTA 1083
1081 TAATCAGAAAATAACTTATTTCTTAATCAGAAAGCAGTACAAAAGAAAGTAAATATGTTT 1140
1084 TAATCAGAAAATAACTTATTTCTTAATCAGAAAGCAGTACAAAAGAAAGTAAATATGTTT 1143
1141 TATAAGATTTAGAGTTAAGTAAAGTTTAAAGCTTTTGCAAAAGTTGTCAAAAGTTCAACA 1200
1144 TATAAGATTTAGAGTTAAGTAAAGTTTAAAGCTTTTGCAAAAGTTGTCAAAAGTTCAACA 1203
1201 AAAGTCTAGTTGGGATTTTACCAAGCAGCATATATGTTTATATAAATCAATATATAT 1260
1204 AAAGTCTAGTTGGGATTTTACCAAGCAGCATATATGTTTATATAAATCAATATATAT 1263
1261 ACTCAGATATCCAAATGTTTCAGATAGCATTTTTCATATGATGTTCTCTTTTTCGTT 1320
1264 ACTCAGATATCCAAATGTTTCAGATAGCATTTTTCATATGATGTTCTCTTTTTCGTT 1323
1321 AATAGTGAAGATGATGTTGTTCTTAATGGGAGATGAAGAAATTTATTTATTTGGTT 1380
1324 AATAGTGAAGATGATGTTGTTCTTAATGGGAGATGAAGAAATTTATTTATTTGGTT 1383
1381 ACTACTAACCTCTGCCAAGATAGTAAATATCCTCTAGTTTAAAGCCAGCAACAGGAA 1440
1384 ACTACTAACCTCTGCCAAGATAGTAAATATCCTCTAGTTTAAAGCCAGCAACAGGAA 1443
1441 CTTTGTGGAAGACATATTCATCTTACAGAACTTCAGATTAATATATCTAGATTAATG 1500
1444 CTTTGTGGAAGACATATTCATCTTACAGAACTTCAGATTAATATATCTAGATTAATG 1503
1501 ACTGAAATAGATCCACATTTGAACTTCTTCTTAAAGTGAACATGAGTACCCAGTTAT 1560
1504 ACTGAAATAGATCCACATTTGAACTTCTTCTTAAAGTGAACATGAGTACCCAGTTAT 1563
1561 ACAAAGTACTTCTGTTGGTCACAGAAACATGACCAAGATTTTTCATATCTCCAGGTAGGGA 1620

1564 ACAAGTACTTCTGTTGGTCACAGAAACATGACCAGATTTTGCATATCTCCAGGTAGGA 1623
1621 ACTAAGTAGACTACCTTATCAGCCGGTAAAGAAAATTTGCTACTAAACTTATTTAGGCCATCA 1680
1624 ACTAAGTAGACTACCTTATCAGCCGGTAAAGAAAATTTGCTACTAAACTTATTTAGGCCATCA 1683
1681 ATGGCTTGATTAACCAACAGAGAGGTTTTCAGGAGCTCTCATGTTTGGCCCTTTAG 1740
1684 ATGGCTTGATTAACCAACAGAGGTTTTCAGGAGCTCTCATGTTTGGCCCTTTAG 1742
1741 AATTGGGGTAGAATCAGAAATGAGATGAGGGGAAGCAAGAGGAGTCTAAGGCCCTAGC 1800
1743 AATTGGGGTAGAATCAGAAATGAGATGAGGGGAAGCAAGAGGAGTCTAAGGCCCTAGC 1802
1801 GATTGGGCATCTGCCACATTTGGTTTCATATTCAGAAAG 1838
1803 GATTGGGCATCTGCCACATTTGGTTTCATATTCAGAAAG 1840

RESULT 6

AA518331
ID AA518331 standard; cDNA; 1486 BP.

XX AA518331;

XX AC

XX XX

XX 12-MAR-2002 (first entry)

XX cDNA from a human thyroid library encoding C-terminal region of RGS18.

XX Human; regulator of G protein signalling; RGS18; arterial thrombosis;

XX platelet activation dysfunction; myocardial infarction; stroke;

XX coronary artery disease; cerebrovascular disease; unstable angina;

XX deep vein thrombosis; systemic thrombosis; anti-coagulant;

XX invasive cardiac procedure; thyroid; ss.

XX Homo sapiens.

XX Key

XX CDS

XX Location/Qualifiers

XX 3. .212

XX /*tag= a

XX /partial

XX /product= "Carboxy-terminal region of RGS18"

XX /note= "this sequence lacks a start codon"

XX WC200183514-A2.

XX 08-NOV-2001.

XX 26-APR-2001; 2001WO-US013540.

XX 28-APR-2000; 2000US-0200786P.

XX 02-AUG-2000; 2000GS-00018833.

XX (AVET) AVENTIS PHARM PROD INC.

XX Murray DL, Gagnon AW;

XX WPI; 2002-055453/07.

XX P-PSDB; AAU10748.

XX Isolated regulator of G protein signalling polypeptide, useful for prevention/treatment of platelet activation dysfunction, such as arterial thrombosis, myocardial infarction, coronary artery disease and stroke.

XX Example 2; Page 113-114; 127pp; English.

XX The present invention relates to the isolation of polynucleotide sequences, that encode a novel regulator of G protein signalling (RGS) polypeptide, RGS18, from human platelets. The invention also provides nucleotide primers and probes specific for an RGS18 nucleic acid. The sequences of the invention are useful for the manufacture of a medicament for the prevention or treatment of a platelet activation dysfunction,

CC such as arterial thrombosis, myocardial infarction, coronary artery
CC disease, stroke, cerebrovascular disease, unstable angina, deep vein
CC thrombosis, systemic thromboembolism, and in invasive cardiac procedures
CC for anti-coagulant purposes. The sequences of the invention can also be
CC used for the detection of RGS18 nucleic acids and RGS18 polypeptides. The
CC present sequence represents a cDNA sequence from an Incyte clone derived
CC from a human thyroid library. The sequence is used to isolate the full
CC length cDNA encoding RGS18 from human platelets
XX
SQ Sequence 1486 BP; 529 A; 235 C; 240 G; 482 T; 0 U; 0 Other;

Query Match 65.3%; Score 1448.2; DB 6; Length 1486;
Best Local Similarity 99.4%; Pred. No. 2.4e-249;
Matches 1464; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 656 CTCACCTACCTCCACAGTTTCTGAAATCTGACATCTATTAGACTTGTGGAAGGAGAC 715
DB 1 CTCACCTACCTCCACAGTTTCTGAAATCTGACATCTATTAGACTTGTGGAAGGAGAC 60
QY 716 AAGACAGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTGTGGAAGGAGAC 775
DB 61 AAGACAGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTGTGGAAGGAGAC 120
QY 776 CTCAGAGACCAACAATCTTAGAGAGCATACGGTCAATTTACCTGCAATGAATPCCAAG 835
DB 121 CTCAGAGACCAACAATCTTAGAGAGCATACGGTCAATTTACCTGCAATGAATPCCAAG 180
QY 836 ATGTCAATCAGATGTCGCAATTTGGTTATAGAAATGATTTGCTCAATTTTATGA 895
DB 181 AAGTCAATCAGATGTCGCAATTTGGTTATAGAAATGATTTGCTCAATTTTATGA 240
QY 896 CAAACTTATACATCTGCTTCTAACATATCGCATGTTTATGTTAAGATTGGTCCCATCCT 955
DB 241 CAAACTTATACATCTGCTTCTAACATATCGCATGTTTATGTTAAGATTGGTCCCATCCT 300
QY 956 TTAACCTGCAATATGCTGTGGAATTTTAAATGTAACAAACAACTTCTGCTA 1015
DB 301 TTAACCTGCAATATGCTGTGGAATTTTAAATGTAACAAACAACTTCTGCTA 360
QY 1016 ACAAATACATACAGTATCTGCCAGTATCTGTAACACCTTCTATTGATGCAITCC 1075
DB 361 ACAAATACATACAGTATCTGCCAGTATCTGTAACACCTTCTATTGATGCAITCC 420
QY 1076 ATTTATATCAGAAAAAATCTTATTTCTTAATCAAAAGGCGATACAAAAAAGTATATA 1135
DB 421 ATTTATATCAGAAAAAATCTTATTTCTTAATCAAAAGGCGATACAAAAAAGTATATA 480
QY 1136 TGTTTTAAAGATTGTAGAGTTAAGTAAAGTTTGAAGTTTGCAGAAAGTTTC 1195
DB 481 TGTTTTAAAGATTGTAGAGTTAAGTAAAGTTTGAAGTTTGCAGAAAGTTTC 540
QY 1196 AAACAAAAGTCTAGTTGGGATTTTTCACAAAGCAGCATATATGTGTTATATAACATA 1255
DB 541 AAACAAAAGTCTAGTTGGGATTTTTCACAAAGCAGCATATATGTGTTATATAACATA 600
QY 1256 ATAATACACAGATATCCAAATGTTTCAGATACGATTTTTCATATGAATGTTCTTTTT 1315
DB 601 ATAATACACAGATATCCAAATGTTTCAGATACGATTTTTCATATGAATGTTCTTTTT 660
QY 1316 TTGTTAATAGTTAGAGTTGATCTGTTCTTACAAATGGGAGATGAAGAACATTTATTATT 1375
DB 661 TTGTTAATAGTTAGAGTTGATCTGTTCTTACAAATGGGAGATGAAGAACATTTATTATT 720
QY 1376 GGGTTACTACTAACCTGTCCCAAGATAGTATATACCTCTAGTTATAGCCAGCAAC 1435
DB 721 GGGTTACTACTAACCTGTCCCAAGATAGTATATACCTCTAGTTATAGCCAGCAAC 780
QY 1436 AGGAACCTTTTGTGAAGACACATTTCTCTACAGAACTTCAGATTAAATATAATCTAGAT 1495
DB 781 AGGAACCTTTTGTGAAGACACATTTCTCTACAGAACTTCAGATTAAATATAATCTAGAT 840
QY 1496 TAATGACTGAGATTAAGATPCCATTTTGAACCTCATTTCTTAAGTGAACATGACGTACCCA 1555

DB 841 TAATGACTGAGATAAGATCCACATTTGAATCTATTCTTAAGTGAACATGACGTACCCA 900
QY 1556 GTTATACAAAGTACTTCTGTGTGTACAGAAAAATGACCAAGATTTGTCATATCTCCAGGT 1615
DB 901 GTTATACAAAGTACTTCTGTGTGTACAGAAAAATGACCAAGATTTGTCATATCTCCAGGT 960
QY 1616 AGGGAACCTAAGTAGACATACCTTATACCCGGCTAAGAAAACTTCTACTAACTATTAGGC 1675
DB 961 AGGGAACCTAAGTAGACATACCTTATACCCGGCTAAGAAAACTTCTACTAACTATTAGGC 1020
QY 1676 CATCAATGGCTTGAATAAAAACCCAGAGAAAGTTTTCAGAGGACGTTCTCATGTTGGCCC 1735
DB 1021 CATCAATGGCTTGAATAAAAACCCAGAGAAAGTTTTCAGAGGACGTTCTCATGTTGGCCC 1079
QY 1736 TTTAGAAATGGGCTAGAAATCAGAAATGAGATGAGGGGAGAGCAAGGAGTCTTAGGCC 1795
DB 1080 TTTAGAAATGGGCTAGAAATCAGAAATGAGATGAGGGGAGAGCAAGGAGTCTTAGGCC 1139
QY 1796 CTAGCGATTTGGGCATCTGCCACATTTGGTTTCATATTCAGAAAGTGTATCTCATTTGATTA 1855
DB 1140 CTAGCGATTTGGGCATCTGCCACATTTGGTTTCATATTCAGAAAGTGTATCTCATTTGATTA 1199
QY 1856 TATCTTGTTAAGCAATCTCCTTAAGTAATTAATTAATTAAGTAATTAATTAATTAATTAATTA 1915
DB 1200 TATCTTGTTAAGCAATCTCCTTAAGTAATTAATTAATTAAGTAATTAATTAATTAATTAATTA 1259
QY 1916 TCTATATGTCACGTGTTTAAAGAGATATTTAAATTTTAAATGTTGTGTACATGTTCTGTAA 1975
DB 1260 TCTATATGTCACGTGTTTAAAGAGATATTTAAATTTTAAATGTTGTGTACATGTTCTGTAA 1319
QY 1976 ATATTTGTTATTTAAAAATGCCATGCAATAGGCTTTGGAAATTTAAATTTAGTTGAAATGT 2035
DB 1320 ATATTTGTTATTTAAAAATGCCATGCAATAGGCTTTGGAAATTTAAATTTAGTTGAAATGT 1379
QY 2036 ABAATGTGAAACCTTTAGATCATTTCTAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 2095
DB 1380 ABAATGTGAAACCTTTAGATCATTTCTAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 1439
QY 2096 TAAATTTATCTGACATTAAGGCTCTGACTGAA 2128
DB 1440 TAAATTTATCTGACATTAAGGCTCTGACTGAA 1472

RESULT 7
ABQ98617
ID ABQ98617 standard; DNA; 848 BP.
XX AC ABQ98617;
XX AC ABQ98617;
DT 04-NOV-2002 (first entry)
XX Human ORF424 coding sequence.
XX Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary;
XX Antiinflammatory; gene therapy; human; ORP; atherogenic; platelet;
XX human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;
XX cancer; cardiovascular disease; allergy; autoimmune disease;
XX wound healing; blood coagulation disorder; inflammatory disorder; ds.
XX Homo sapiens.
XX OS
XX US2002082206-A1.
PN 27-JUN-2002.
XX
PD 30-MAY-2001; 2001US-00867550.
XX
PF 30-MAY-2000; 2000US-0208427P.
XX
PR (LEAC/) LEACH M D.
XX (MEHR/) MEHRBAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.

QY 547 CAAATTCACCTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAAA 606
 DB 61 CAAATTCACCTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAAA 120
 QY 607 GAGGTTAACTGATTTTACACAAAAGAGTCATTACAAAAGAGTCACTCAACCTACC 666
 DB 121 GAGGTTAACTGATTTTACACAAAAGAGTCATTACAAAAGAGTCACTCAACCTACC 180
 QY 667 CTCCACAGTTTGTGCTGCACAAAGCAGAGTGTATCAGCTCATGGACAGACAGTTAT 726
 DB 181 CTCCACAGTTTGTGCTGCACAAAGCAGAGTGTATCAGCTCATGGACAGACAGCTAT 240

RESULT 11
 ACC43243
 ID ACC43243 standard; DNA; 408 BP.
 XX
 AC ACC43243;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Nucleotide sequence of regulator polypeptide of G-protein signalling.
 XX
 KW Human; regulator polypeptide of G-protein signalling; RGS; chromosome 1;
 KW asthma; diabetes; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 4. 408
 FT /*tag= a
 FT /product= "regulator polypeptide of G-protein signalling"
 XX
 FN WO2003016345-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 16-AUG-2002; 2002WO-EP009173.
 XX
 PR 16-AUG-2001; 2001US-0312345P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Koehler RH;
 XX
 WPI; 2003-278547/27.
 DR P-PSDB; ABP98021.
 XX
 PT New polynucleotide encoding a regulator polypeptide of G-protein
 PT signaling (RGS) and RGS protein, useful in gene therapy to modulate the
 PT activity of RGS in a disease, particularly in asthma or diabetes.
 XX
 PS Claim 1; Fig 4; 99pp; English.
 XX
 CC The present sequence encodes an alternatively spliced version of human
 CC regulator polypeptide of G-protein signaling (RGS). The RGS gene is
 CC located on chromosome 1. The RGS polynucleotide and polypeptide are
 CC useful for identifying test compounds, that may act as agonists or
 CC antagonists at the receptor site and which can be regulated to provide
 CC therapeutic effects. The polynucleotide, polypeptide or vectors
 CC comprising the polynucleotide, and the reagents are useful for modulating
 CC the activity of RGS in a disease, particularly in asthma or diabetes
 XX
 SQ Sequence 408 BP; 139 A; 77 C; 77 G; 115 T; 0 U; 0 Other;

Query Match 7.1%; Score 158.4; DB 7; Length 408;
 Best Local Similarity 63.8%; Pred. NO. 3.8e-19;
 Matches 240; Conservative 0; Mismatches 136; Indels 0; Gaps 0;
 QY 389 CTGAAGGCGCAGTGAATGGGTGAATCATTTGACAACTGCTTCCCATAGACATGAC 448
 DB 17 CTGCGGAACATGACATGGTCTGAAATATGGACACCGCTTTAGCCAAACCAAGCTGGTC 76

QY 449 TAGAGGCTTTTACCAGATTTCTTAAAACTGAATTCAGTGAAGAAAAATATTGAATTTGGA 508
 DB 77 TAGATGCTTTTCGAAATATTTCTAAAAATCAGAGTTTAGTGAAGAAAAATGTTGAGTCTGGC 136
 QY 509 TAGCCTGTGAAGATTTCAAGAAAAAGCAAGGACCTCAACAAATTCACCTTAAAGCAAAAG 568
 DB 137 TTGCCTGTGAAGCTTTTAAGAAAAAGCAAAATGAGACAAAATGCTTCCAAAGCCAGA 196
 QY 569 CAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACTTGATTTTCA 628
 DB 197 TGAATTTATCTGAAATTCATTGAAGCTGATGCACCTAAAGAGATTAACATTGACTTCGGTA 256
 QY 629 CAAAAGAAAGTCATTACAAAAGACATCACTCAACCTACCCTCCACAGTTTGTATCTGCAC 688
 DB 257 CCAGAGACCTCATCTCAAGAAATATTCCTGAACCAACACTCAAAATGCTTTGATGAGGCTC 316
 QY 689 AAAGCAGAGTGTATCAGCTCATGGACAAAGACAGATTATACACAGTTTCTGAAATCTGACA 748
 DB 317 AGAAATTAATCTATTGTCTCATGGCCCAAGGATTTCTTCCCTCGATTTCTGAAGTCAGAGA 376
 QY 749 TCTATTTAGACTTGAT 764
 DB 377 TTATATAAAACTGGT 392

RESULT 12
 AAH76414
 ID AAH76414 standard; cDNA; 1795 BP.
 XX
 AC AAH76414;
 XX
 DT 04-OCT-2001 (first entry)
 XX
 DE RGS protein 17 cDNA.
 XX
 KW RGS protein 17; cytostatic; virucidal; immunomodulatory;
 KW antiinflammatory; haemostatic; cancer; haemopathy; infection;
 KW human immunodeficiency virus; HIV; immunological disease;
 KW inflammatory disease; ss.
 XX
 OS Unidentified.
 XX
 PN WO200155414-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 15-JAN-2001; 2001WO-CN000032.
 XX
 PR 26-JAN-2000; 2000CN-00111515.
 XX
 PA (BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 WPI; 2001-476216/51.
 DR P-PSDB; AAG66509.
 XX
 PT RGS protein 17 and encoded polynucleotide, applicable in diagnosis and
 PT treatment of malignant tumor, hemopathy, HIV infection, immunological
 PT diseases and various inflammations.
 XX
 PS Claim 6; Page 29-30; 35pp; Chinese.
 XX
 CC The invention relates to an isolated polypeptide of RGS protein 17
 CC comprising the 152 amino acid sequence defined in the specification, or
 CC its fragment, analogue or derivative. The polypeptide and the
 CC polynucleotide encoding it are useful in the diagnosis and treatment of
 CC malignant tumours, haemopathy, HIV infection, immunological diseases and
 CC various inflammatory diseases. The present sequence encodes the
 CC polypeptide of the invention
 XX
 SQ Sequence 1795 BP; 632 A; 295 C; 281 G; 587 T; 0 U; 0 Other;

Query Match	7.13;	Score 158.4;	DB 4;	Length 1795;
Best Local Similarity	63.8;	Pred. No. 4.4e-19;		
Matches 240;	Conservative 0;	Mismatches 136;	Indels 0;	Gaps 0;
QY	389	CTGAAAGGCGAGTGAATGGGTGAACTCATTTCACAAACTGCTTTCCCATAGAGATGCAC	448	
Db	210	CTGCGGAACCAATGACATGCTCTGAAAATATGACACGCTTTTAGCCACCAAGCTGGTC	269	
QY	449	TAGAGGCTTTTACCAGAGTTTCTTTAAAACTGAAATTCAGTGAAGAAAAATATTGGAATTTTGGAA	508	
Db	270	TAGATGCTTTTTCGAATATTTCTAAATACAGAGTTTAGTGAAGAAAAATGTTGAGTTCTGGC	329	
QY	509	TAGCCTGTGAGATTTCAAGAAAGCAGGGAGCTCAACAAATTCACCTTTAAAGCAAAAG	568	
Db	330	TGCGCTGTGAAGAGCTTTAAGAAAAACGAAAAATGCGACAAATTTGCTTCCAAAGCCAAAGA	389	
QY	569	CAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACTTTGATTTTTCACA	628	
Db	390	TGATTTTATTCAGATTCATTGAAGCTGATGCACCTAAAGAGATTAACATTGACTTCGGTA	449	
QY	629	CAAAAGAGTCAATTACAAAGAGATCACTCAACTACCTCCACAGTTTTTGATGCTGCAC	688	
Db	450	CCAGAGACCTCATCTCAAAGAATATTGCTGAACCAACACTCAAAATGCTTTGATGAGGGTTC	509	
QY	689	AAAGCAGAGTGTATCAGCTCATCGAAACAAGACAGTTATACACGTTTTCTGAAATCTTGACA	748	
Db	510	AGAAATTAATCTATTGCTCTATGGCCAGGATTTCTTCCCTCGATTTCTGAAGTCAGAGA	569	
QY	749	TCTATTAGACTTGAT	764	
Db	570	TTTATAAAAAAAGTGGT	585	

RESULT 13

ABT10881
ID ABT10881 standard: cDNA: 1345 BP.

XX
AC
ART10881:XX
DT 04-DEC-2002 (first entry)

XX DE Human breast cancer associated coding sequence SEO ID NO: 1015.

Human; breast specific gene; breast cancer; differential expression;
KW
XX
XX
kw cytostatic; gene therapy; gene; ss.
kw

XX Homo sapiens.

XX PN WO200259271-A2.

XX PD 01-AUG-2002.

XX
PF 25-JAN-2002; 2002WO-US002176.

XX
PR 25-JAN-2001: 2001US-0263757P.

PR 25-APR-2001; 2001US-0286090P.
PR 23-MAY-2001; 2001US-0292517P.

XX (GENE-) GENE LOGIC INC
PA[illegible]

XX
DE WPT: 3002-574803/72

XX
PT
diagnosing breast ca

PT gene expression in cell or tissue samples, where a differential gene expression is indicative of breast cancer.

XX
PS
Claim 1: SEQ ID NO 1015: 260pp + Sequence Listing; English.

XX The present invention relates to methods of diagnosing breast cancer in a
CC patient, which comprise detecting the level of expression in a tissue
CC sample of two or more genes selected from those shown in ABR09867-
CC

ABT1112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://www.wipo.int/pub/pct/publicat/pct_sequences](http://www.wipo.int/pub/pct/publicat/pct_sequences)

XX
Sequence 1345 BP: 443 A; 254 C; 304 G; 344 T; 0 U; 0 Other;

Query Match	7.0%;	Score 155.6;	DB 6;	Length 1345;
Best Local Similarity	63.2%;	Pred. No. 1.4e-18;		
Matches 319:	Conservative	0:	Mismatches 139:	Indels 0;

385	QY	TCCCTCGAAGGCAGTGAATCGGGTGAATCATTTTGACAAACTGCTTCCCATAGAGAT	444
249	Db	TCTCTCGAGGAAGCACACAGCTGTGGTCAGAAGCATTTTGCAGGAGCTGTGACGCCAGCAAAATAT	308
445	QY	GGACTAGAGGCTTTTACCAGATTCTTAAACCTGAATTCAGTGAAGAAATATTGAAATTT	504
309	Db	GGTCTTGCTGCAITCAGGGCTTTTAAAGTCGGAAATCTGTGAGAAATATTGAAATTC	368
505	QY	TGGATAGCCTGTGAAGATTTCAAGAAAAAGCAAGGACCTCAACAAATTCACCTTAAAGCA	564
369	Db	TGGCTGGCTGTGAAGACTTCAAAAAAOCCTCAACCCAAAGGTGTCCTCAAAAGCA	428
565	QY	AAAGCAATATATGAGAAATTTTACAGACTGATGCCCAAAAGAGGTTAAACCTTGATTT	624
429	Db	AGGAAATATATACTGACTTTCATAGAAAGGAAGCTCCAAAAGAGATAAACATAGATTT	488
625	QY	CACACAAAGAGGTCATTACAAACAGCATCACTCAACCTACCCCTCACAGTTTTGATGCT	684
489	Db	CAAAACCAAACTGTGATTGCCCGAATATACAGAGAGCTACAAGTGGCTGCTTTACAACT	548
685	QY	GCACAAAGCAGAGTGTATCAGCTCATGAAACAAGACAGTTTATACAGTTTTTCTGAAATCT	744
549	Db	CCCCAGAAAGGTAATACAGTTGATGAGAGAACAACTCTTATCCTCGTTCTTGAGGATCA	608
745	QY	GACATCTATTTAGACTTG	762
609	Db	GAATTCCTACGAGGACTTG	626

RESULT 14

ABK83834
ID ABK83834 standard. CDNA: 1345 BP.

XX
AC ABX83834.

XX
DT 14-AUG-2002 (first entry)

XX
DE Human cDNA differentially expressed in granulocytic cells #405.

Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; streptococcal inflammatory disease; psoriasis; rheumatoid arthritis; hemangioendothelioma; thrombosis; salivary gland infection; renal reperfusion injury; AIDS; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

XX
50 Homo sapiens.

XX
PN
WO200228999-A2.XX
11-APR-2002.

Db	309	GGTCTTGCTGCATTGAGGGCTTTTAAAGTCGGAATTCGTGAAGAAAATATTGAATTC	368
Qy	505	TGGATAGCCTGTGAGATTTCAGAGAAAGCAAGGACCTCAACAAATTCACCTTAAAGCA	564
Db	369	TGGCTGGCTGTGAGACTTCAAAAAACCAATCACCCAAAAGCTGCTCATAAGCA	428
Qy	565	AAAGCAATATATGAGAAATTTATACAGACTGATGCCCCAAAAGAGTTAACCTTGATTTT	624
Db	429	AGGAAATATATATCTGACTTCATAGAAAAGGAGCTCCAAAAGAGATAAACATAGATTTT	488
Qy	625	CACACAAAAGAGTCATTACAAACAGCATCACTCACTACCTCCCTCCACAGTTTGTGCT	684
Db	489	CAACCCAAACTCTGATTCGCCAGATATACAGAGCTCAAGTGGCTGCTTTACAACT	548
Qy	685	GCACAAAGCAGAGTGTATCAGCTCATGGAACAAGACAGTTATACACGTTTCTGAAATCT	744
Db	549	GCCCAAGAAAGGTATACAGCTTGATGAGAACAACTCTTATCCTCGTTTCTTGGAGTCA	608
Qy	745	GACATCTATTTAGACTTG	762
Db	609	GAATCTACAGGACTTG	626

Search completed: August 20, 2004, 06:15:33
Job time : 928.824 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2217	100.0	2217	3	US-09-244-314-1	Sequence 1, Appli
2	2217	100.0	2217	4	US-09-498-959-1	Sequence 1, Appli
3	596	26.9	1164	3	US-09-244-314-3	Sequence 3, Appli
4	596	26.9	1164	4	US-09-498-959-3	Sequence 3, Appli
5	388	17.5	736	4	US-09-833-381-1010	Sequence 1010, Ap
6	155.6	7.0	1345	4	US-09-016-434-1278	Sequence 1278, Ap
7	155.6	7.0	1345	4	US-09-023-655-1243	Sequence 1243, Ap
8	153.2	6.9	744	2	US-08-748-483-2	Sequence 2, Appli
9	153.2	6.9	2190	4	US-09-023-655-795	Sequence 795, App
10	146.6	6.6	3208	4	US-09-566-921-111	Sequence 111, App
11	143.8	6.5	800	4	US-09-016-434-1091	Sequence 1091, Ap
12	141.2	6.4	1398	4	US-09-016-434-1290	Sequence 1290, Ap
13	141.2	6.4	1398	4	US-09-702-705-322	Sequence 322, App
14	141.2	6.4	1398	4	US-09-736-457-332	Sequence 322, App
15	141.2	6.4	1398	4	US-09-614-124B-322	Sequence 322, App
16	141.2	6.4	1398	4	US-09-671-325-332	Sequence 322, App
17	141.2	6.4	1398	4	US-09-589-184-332	Sequence 332, App
18	127	5.7	2638	4	US-09-016-434-1090	Sequence 1090, Ap
19	115.8	5.2	606	2	US-08-463-081B-27	Sequence 27, Appl
20	115.8	5.2	606	2	US-08-461-379A-27	Sequence 27, Appl
21	115.8	5.2	606	2	US-08-463-330B-27	Sequence 27, Appl
22	115.8	5.2	606	3	US-08-463-074B-27	Sequence 27, Appl
23	115.8	5.2	606	3	US-08-465-595C-27	Sequence 27, Appl
24	115.8	5.2	606	3	US-08-652-446-27	Sequence 27, Appl
25	115.8	5.2	746	3	US-08-870-815-3	Sequence 3, Appli
26	115.8	5.2	746	3	US-08-949-004-3	Sequence 3, Appli
27	115.8	5.2	2383	1	US-08-274-318-1	Sequence 1, Appli

; NAME/KEY: CDS									
; LOCATION: (160)...(867)									
US-09-498-959-1									
Query Match 100.0%; Score 2217; DB 4; Length 2217;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GAATCGGCTTCATCCTTAATACGACTCACTATAGGGCTCGAGCGCGCGCGCGGCGAGGT	60						
DB	1	GAATTCGGCTTCATCCTTAATACGACTCACTATAGGGCTCGAGCGCGCGCGCGGCGAGGT	60						
QY	61	ATAACCTTTTATTCTACTATGATATGATGGAATAGTATTAAATAAGTAACTAGGGAAG	120						
DB	61	ATAACTTTTATTCTACTATGATATGATGGAATAGTATTAAATAAGTAACTAGGGAAG	120						
QY	121	GATGTAATAAATAGACATCTCTTCAATTTTAGAGAGAAGTGAACAAACATCTCTTTTC	180						
DB	121	GATGTAATAAATAGACATCTCTTCAATTTTAGAGAGAAGTGAACAAACATCTCTTTTC	180						
QY	181	TTTTCTCAATAAATATGTCGAATCAAAAGAAAAAATCTTTTCAAGTTTAATACATGGT	240						
DB	181	TTTTCTCAATAAATATGTCGAATCAAAAGAAAAAATCTTTTCAAGTTTAATACATGGT	240						
QY	241	TCAGAAAAAGAGAAACAAGCAAAAGAGCGCAAAATCAGAGCTTAAGAAAAAGAAATAGA	300						
DB	241	TCAGAAAAAGAGAAACAAGCAAAAGAGCGCAAAATCAGAGCTTAAGAAAAAGAAATAGA	300						
QY	301	CTAAGTCTCTTCTGTGCAGAAACCTGAGTTTCATGAAAGACACCCGCTCAGTAGATCTGGG	360						
DB	301	CTAAGTCTCTTCTGTGCAGAAACCTGAGTTTCATGAAAGACACCCGCTCAGTAGATCTGGG	360						
QY	361	CACCTGGCAAAAGAAACAAGAGTCTCCCTGAAGAGGCGAGTGAATGGGTGAATCAATTT	420						
DB	361	CACCTGGCAAAAGAAACAAGAGTCTCCCTGAAGAGGCGAGTGAATGGGTGAATCAATTT	420						
QY	421	GACAAACTGCTTTCCCATAGAGATGGAATAGAGGCTTTTACAGATTTCTTTAAACTGAA	480						
DB	421	GACAAACTGCTTTCCCATAGAGATGGAATAGAGGCTTTTACAGATTTCTTTAAACTGAA	480						
QY	481	TTCAAGTGAAGAAATATTCGAATTTTGGATAGCGCTGTGAAGATTTCAAGAAAGCAAGGA	540						
DB	481	TTCAAGTGAAGAAATATTCGAATTTTGGATAGCGCTGTGAAGATTTCAAGAAAGCAAGGA	540						
QY	541	CCTCAACAAATTCACCTTAAAGCAAAAGCAATATATAGAAATTTATACAGACTGATGCC	600						
DB	541	CCTCAACAAATTCACCTTAAAGCAAAAGCAATATATAGAAATTTATACAGACTGATGCC	600						
QY	601	CCAAAGAGGTTAACTTGAATTTTACACAAAGAGTCAATACAAACAGCATCACTCAA	660						
DB	601	CCAAAGAGGTTAACTTGAATTTTACACAAAGAGTCAATACAAACAGCATCACTCAA	660						
QY	661	CCTTACCCTCCACAGTTTTCATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAAGAC	720						
DB	661	CCTTACCCTCCACAGTTTTCATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAAGAC	720						
QY	721	AGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTTAGAGTGAAGAGGACCTCAG	780						
DB	721	AGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTTAGAGTGAAGAGGACCTCAG	780						
QY	781	AGACCAACAAATCTTAGGAGAGCATCAGCTCAATTTTACCTGCAATGAAATCCCAAGATGTA	840						
DB	781	AGACCAACAAATCTTAGGAGAGCATCAGCTCAATTTTACCTGCAATGAAATCCCAAGATGTA	840						
QY	841	CAATCAGATGTTGCCATTTGGTTATAAGAAAAATTTGATTTTCTCATTTTATGACAAAC	900						
DB	841	CAATCAGATGTTGCCATTTGGTTATAAGAAAAATTTGATTTTCTCATTTTATGACAAAC	900						
QY	901	TTATACATCTGCTTCTAACATATCCGATGTTTATGTTAAGATTTGGTCCCATCTTTAA	960						
DB	901	TTATACATCTGCTTCTAACATATCCGATGTTTATGTTAAGATTTGGTCCCATCTTTAA	960						
QY	961	CTGAAATATGCTATGTAATTTATTTTAAATATGTAAGAACTTTCTGCTAAACAA	1020						

QY 187 CAATAAATATGTGTGAATCAAAAGAAAAAATTTTCAAGTTAATACATGTTTACGGA 246
Db 161 CAATTAATATGTGTGAATCAAAAGAAAAAATTTTCAAGTTAATACATGTTTACGGA 220
QY 247 AAAGAGAAACAAAGCAAGAACCCAAATCAGAGTAAAGGAAAAAGAAATAGACTAAGT 306
Db 221 AAAGAGAAACAAAGCAAGAACCCAAATCAGAGTAAAGGAAAAAGAAATAGACTAAGT 280
QY 307 CTTCTTGTGAGAAACCTGAGTTTCATGAAGACACCCCTCCAGTAGATCTGGGCACTTG 366
Db 281 CTTCTTGTGAGAAACCTGAGTTTCATGAAGACACCCCTCCAGTAGATCTGGGCACTTG 340
QY 367 GCCAAGAAAAAAGAGTCTCCCTCAAGAGGAGTGAATGGGTGAATCATTTGACAAA 426
Db 341 GCCAAGAAAAAAGAGTCTCCCTCAAGAGGAGTGAATGGGTGAATCATTTGACAAA 400
QY 427 CTGCTTCCCATAGAGTGAAGTCTAGAGCTTTTACAGATTTCTTAAATCAATTCAGT 486
Db 401 TTGCTCTCTCATAGAGTGAAGTCTAGAGCTTTTACAGATTTCTTAAATCAATTCAGT 460
QY 487 GAAGAAATATGAAATTTGGATAGCTGTGAAGATTTCAAGAAAGCAAGGACCTCAA 546
Db 461 GAGGAGAACATTTGATTTGGTGTGCTGTGAAGATTTCAAGAAAGCAAGGACCTCAA 520
QY 547 CAATTTCACTTAAAGCAAAAGCAATATATAGAGAAATTTATACAGACTGTGCCCCAAA 606
Db 521 CAATTTCACTTAAAGCAAAAGCAATATATAGAGAAATTTATACAGACTGTGCCCCAAA 580
QY 607 GAGGTTAAGCTGATTTTACACAAAAGAGTCAATACAAAGAGTCACTCAACCTACC 666
Db 581 GAGGTTAAGCTGATTTTACACAAAAGAGTCAATACAAAGAGTCACTCAACCTACC 640
QY 667 CTCCACAGTTTGTGCTGCAAAAGCAGAGTGTATCAGCTCATGGAACAAAGACAGTTAT 726
Db 641 CTCCACAGTTTGTGCTGCAAAAGCAGAGTGTATCAGCTCATGGAACAAAGACAGTTAT 700
QY 727 ACAGTTTCTGAAATCTGACATCTATTAGACTGTGGAAGAAAGACCTCAGAGACCA 786
Db 701 AAACGCTTTTGAATCTGAGACCTACTTACATTTGATAGAAGAAAGACCTCAGAGACCA 760
QY 787 ACAGATCTAGAGACGATCAGCTCATTTACCTGCAATGAATTTCAAGAGTGAATCA 846
Db 761 ACAGATCTAGAGACGATCAGCTCATTTACCTGCAATGAATTTCAAGAGTGAATCA 820
QY 847 GATGTTGCCATTGTTTAAAGAAAAATTTGCTCATTTTATGACAAACCTTATAC 906
Db 821 GATGTTGCCATTGTTTAAAGAAAAATTTGCTCATTTTATGACAAACCTTATAC 880
QY 907 ATC-----TGCTTCAACATATCGCATGTTTATGTTAAGA 941
Db 881 ATCTAAATATATATACTAATACTAATGTGTACTTCTAAATATAGCTTGTATAGAAGA 940
QY 942 TTGTGCTCCATCTTTAAACTGAAATATGTATGTAATTTTAAATATGTAATAAC 1001
Db 941 GATGATTTCAATTT-----TAAATACACATGCAATATATTAATGTAAGACTT 994
QY 1002 AAAACTTTCTGTAACAAATATACATAGTATCTGCCAGTATTTCTGTAACCTTCTA 1061
Db 995 TTTATATATATATAAAATTAATTCATCATCTATCTCCGAAATATTTTATGAAATCTATC 1054
QY 1062 TTTGATGTCATTCATTTATATATC 1085
Db 1055 TGATATTTCTATCTAATAAATTC 1078

RESULT 5

US-09-833-381-1010
; Sequence 1010, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1010
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(736)
; OTHER INFORMATION: n = A, T, C or G
US-09-833-381-1010

Query Match 17.5%; Score 388; DB 4; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.2e-73;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTCAGTCAAGAAATATTTGAATTTTGGATAGCTGTGAAGATTTCAAGAAAAAGCAAGGGA 540
Db 4 TTCAGTCAAGAAATATTTGAATTTTGGATAGCTGTGAAGATTTCAAGAAAAAGCAAGGGA 63
QY 541 CCTCAACAAATTCACCTTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGTGCC 600
Db 64 CCTCAACAAATTCACCTTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGTGCC 123
QY 601 CCAAGAGAGTTAACCTTGTATTTTACACAAAAGAGTCAATTAACAAAGCAGTCACTCA 660
Db 124 CCAAGAGAGTTAACCTTGTATTTTACACAAAAGAGTCAATTAACAAAGCAGTCACTCA 183
QY 661 CCTACCTCCACAGTTTGTATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAGAC 720
Db 184 CCTACCTCCACAGTTTGTATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAGAC 243
QY 721 AGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTTGATGGAAGAAAGCCTCAG 780
Db 244 AGTTATACAGTTTCTGAAATCTGACATCTATTAGACTTTGATGGAAGAAAGCCTCAG 303
QY 781 AGACCAACAAATCTTAGGAGACGATCAGCTCATTTACCTGCAATGAATTTCAAGATGA 840
Db 304 AGACCAACAAATCTTAGGAGACGATCAGCTCATTTACCTGCAATGAATTTCAAGATGA 363
QY 841 CAATCAGATTTGCCATTTGGTTATATA 868
Db 364 CAATCAGATTTGCCATTTGGTTATATA 391

RESULT 6

US-09-016-434-1278
; Sequence 1278, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1278:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9292054
US-09-016-434-1278

Query Match 7.0%; Score 155.6; DB 4; Length 1345;
Best Local Similarity 63.2%; Pred. No. 3.3e-24;
Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY	385	TCCCTCTGAAGGCGAGTGAATGGGGTGAATCATTTGACAACTGCTTTCCCATAGAGAT	444
Db	249	TCTCTGAGGAGCAGCTGGTGCAGAGCAITTTGACGAGCTGTAGCCAGCAATAT	308
QY	445	GGACTAGAGGCTTTTACCAGATTTCTTTAAACTGAATTCAGTGAAGAAATATTGAATTT	504
Db	309	GGCTTTGCTGCATTCAGGCGCTTTTAAAGTCGGAATTTCTGTGAAGAAATATTGAATTC	368
QY	505	TGATAGCTGTGAGATTTCAAGAAAGCAGGAGCTCAACAAATTCACCTTAAGCA	564
Db	369	TGGCTGGGCTGTGAAGACTTCAAAAAACCAATCACCCCAAGCTGCTCTCAAGCA	428
QY	565	AAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAGAGGTTTAACTTTGATTTT	624
Db	429	AGGAAATATATCTGACTTCATAGAAAGAGCTCCAAAGAGATAACATAGATTT	488
QY	625	CACACAAAGAGTCAATTACAAACAGCATCTCAACCTACCTCCACAGTTTGTGCT	684
Db	489	CAACCAAACTCTGATTTGCCAGAAATATACAAGAGCTCAAGTGGCTGCTTTCAACT	548
QY	685	GCACAAAGCAGAGTGTATCAGCTCATGGAACAGACAGTTATACAGTTTCTGAAATCT	744
Db	549	GCCGAGAAAGGTATACAGCTGTATGAGAACAACTCTTATCTCTGTTCTTGAGTCA	608
QY	745	GACATCTATTAGACTTG 762	
Db	609	GAATTCACAGACTTG 626	

RESULT 7
US-09-023-655-1243
Sequence 1243, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1243:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9292054
US-09-023-655-1243

Query Match 7.0%; Score 155.6; DB 4; Length 1345;
Best Local Similarity 63.2%; Pred. No. 3.3e-24;
Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY	385	TCCCTCTGAAGGCGAGTGAATGGGGTGAATCATTTGACAACTGCTTTCCCATAGAGAT	444
Db	249	TCTCTGAGGAGCAGCTGGTGCAGAGCAITTTGACGAGCTGTAGCCAGCAATAT	308
QY	445	GGACTAGAGGCTTTTACCAGATTTCTTTAAACTGAATTCAGTGAAGAAATATTGAATTT	504
Db	309	GGCTTTGCTGCATTCAGGCGCTTTTAAAGTCGGAATTTCTGTGAAGAAATATTGAATTC	368
QY	505	TGATAGCTGTGAGATTTCAAGAAAGCAGGAGCTCAACAAATTCACCTTAAGCA	564
Db	369	TGGCTGGGCTGTGAAGACTTCAAAAAACCAATCACCCCAAGCTGCTCTCAAGCA	428
QY	565	AAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAGAGGTTTAACTTTGATTTT	624
Db	429	AGGAAATATATCTGACTTCATAGAAAGAGCTCCAAAGAGATAACATAGATTT	488
QY	625	CACACAAAGAGTCAATTACAAACAGCATCTCAACCTACCTCCACAGTTTGTGCT	684
Db	489	CAACCAAACTCTGATTTGCCAGAAATATACAAGAGCTCAAGTGGCTGCTTTCAACT	548
QY	685	GCACAAAGCAGAGTGTATCAGCTCATGGAACAGACAGTTATACAGTTTCTGAAATCT	744
Db	549	GCCGAGAAAGGTATACAGCTGTATGAGAACAACTCTTATCTCTGTTCTTGAGTCA	608
QY	745	GACATCTATTAGACTTG 762	
Db	609	GAATTCACAGACTTG 626	

RESULT 8
US-08-748-483-2
Sequence 2, Application US/08748483
Patent No. 595314
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.

```

; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0157 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 57362
;
US-08-748-483-2

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Query Match          6.9%; Score 153.2; DB 2; Length 744;
Best Local Similarity 61.6%; Pred. No. 9.3e-24;
Matches 245; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 367 GCCAAGAAACAAAGAGTCTCCCTGAAGAGGAGTGAATGGGTGAATCATTTGACAAA 426
DB 210 GCCAAGACCAGAAAACCTCGTGCAGAGGCCCTGCAGTGGCGGTGATTCCTCGACAAA 269

QY 427 CTGCTTTCCCATAGAGTGGAGTGTATACAGATTTCTTAAACCTGAATTCAGT 486
DB 270 CTCCTGCAGACAACTATGAGTTCGCCAGTTTCAAAAGTTTCTTGAAGTCTGAATTCAGT 329

QY 487 GAAGAAATATTGAATTTGGATACCTGTGAAGATTTCAAGAAAGCAAGGACCTCAA 546
DB 330 GAGGAAACCTTGAAGCAAGCAATATATGAGAAATTTATACAGTGTATGATGCTCCAAA 606

QY 547 CAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGTGTATGATGCTCCAAA 606
DB 390 AAGATGGCTGAGAGGCAAGCAATATATGAGAAATTTATACAGTGTATGATGCTCCAAA 449

QY 607 GAGGTTAACTTTGATTTTCAACAAAAGAGTCAATTAACAAACAGCATCACTCAACCTACC 666
DB 450 GAGGTGAATATTGACCACTTCACTAAGGACATCAATGAAGACCTTGGTGGACCTTCC 509

QY 667 CTCACAGTTTGTGCTGCAAGAGAGAGTGTATGAGTTCATGCTGAGCAAGAGAGTAT 726
DB 510 CTGAGCAGCTTTGACATGGCCGCAAGAAAGATCCATGCGCTTATGAGGAAAGGATTCCTG 569

QY 727 ACACGTTTCTGAAATCTGACATCTATTTAGACTTGTAT 764
DB 570 CCTGCTTTGCGCTCTGAGTCTTATCAGAGTTAAT 607

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RESULT 9
US-09-023-655-795
; Sequence 795, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 795:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2190 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAT03
; CLONE: 696878
;
US-09-023-655-795

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Query Match          6.9%; Score 153.2; DB 4; Length 2190;
Best Local Similarity 61.8%; Pred. No. 1.2e-23;
Matches 245; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 367 GCCAAGAAACAAAGAGTCTCCCTGAAGAGGAGTGAATGGGTGAATCATTTGACAAA 426
DB 210 GCCAAGACCAGAAAACCTCGTGCAGAGGCCCTGCAGTGGCGGTGATTCCTCGACAAA 269

QY 427 CTGCTTTCCCATAGAGTGGAGTGTATACAGATTTCTTAAACCTGAATTCAGT 486
DB 270 CTCCTGCAGAACCACTATGAGTTCGCCAGTTTCAAAAGTTTCTTGAAGTCTGAATTCAGT 329

QY 487 GAAGAAATATTGAATTTGGATAGCTGTGAAGATTTCAAGAAAAGCAAGGACCTCAA 546
DB 330 GAGGAAACCTTGAAGTCTGAGTTCGGATTCCTGAGGATTTCAAGAGATCAAGTCCCTGCC 389

QY 547 CAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGTGTATGATGCTCCAAA 606
DB 390 AAGATGGCTGAGAGGCAAGCAATATATGAGAAATTTATACAGTGTATGATGCTCCAAA 449

QY 607 GAGGTTAACTTTGATTTTCAACAAAAGAGTCAATTAACAAACAGCATCACTCAACCTACC 666
DB 450 GAGGTGAATATTGACCACTTCACTAAGGACATCAATGAAGAACCTTGGTGAACCTTCC 509

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QY 667 CTCACAGTTTGTGCTGCACAAAGCAGAGTGATCAGTCTCATGGAACAAAGACAGTTAT 726
DB 510 CTGACAGCTTTGACATGCGCCGAAAGAAATCCATGCCCTGATGGAAGAAAGATTCTCTG 569
QY 727 ACACGTTTCTGAATCTGACATCTATTATAGACTTGAT 764
DB 570 CCTCGTTTGTGCGCTCTGAGTTTATCAGGAGTTAAT 607

RESULT 10

US-09-566-921-111
; Sequence 111, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debra M.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 111
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 900146.4
US-09-566-921-111

Query Match 6.6%; Score 146.6; DB 4; Length 3208;

Best Local Similarity 62.3%; Pred. No. 3.4e-22;
Matches 230; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 396 GCAGTGAATGGGTGAATCATTTGACAAAGCTGCTTCCCATAGAGATGAGCTAGAGGC 455
DB 320 GGCCTGCGAGTGGCGTGATCTCCGACAACTCTCGAGAACACTATGACACTTGCAG 379
QY 456 TTTTACAGATTTCTTAAACTGAATTCAGTGAAGAAATATTGAATTTGGATAGCGTG 515
DB 380 TTTCAAAGTTTCTTCAAGTCTGAATTCAGTGAAGAAACCTTGAGTTCTGGATTGCG 439
QY 516 TGAAGTTTCAAGAAAGCAAGGACCTCAACAATTCACCTTAAAGCAAGCAATATA 575
DB 440 TGAGGATTAACAAGAGATCAAGTCCCTGCCAAGATGGCTGAGAAGGCAAGCAATTA 499
QY 576 TGAGAAATTTATACAGACTGATGCCCAAGAGGTTAACTTTGATTTTTCACAAAAAGA 635
DB 500 TGAGAAATTTATCAACGAGGCTCTTAAGAGGTGAATATTGACCACTTCACTAAGA 559
QY 636 AGTCAATCAACAGCATCACTCAACCTTACCTCCACAGTTTGTGCTGCAACAGCAG 695
DB 560 CATCAATCAAGAAACCTGGTGAACCTTCCCTGAGCAGCTTTGACATGGCCGCAAG 619
QY 696 AGTGATCAGCTCATCGAACAAGAGAGTTATACAGTTTCTGAAATCTGACATCTATT 755
DB 620 ATCCATGCCCTGATGGAAGAGATTTCTGCTGCTTGTGCGCTCTGAGTTTATCA 679
QY 756 AGACTTTGAT 764
DB 680 GGAGTTAAT 688

RESULT 11

US-09-016-434-1091
; Sequence 1091, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1091:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G1216372
; US-09-016-434-1091

Query Match 6.5%; Score 143.8; DB 4; Length 800;

Best Local Similarity 57.2%; Pred. No. 9.4e-22;
Matches 281; Conservative 0; Mismatches 207; Indels 3; Gaps 1;

QY 277 AGAGCTTAAGGAAAAAGAAATAGACTAAGTCTTTGTGCAAGAAACCTGAGTTTCATGAA 336
DB 140 AGTGCAAGATATGAACATCGGCTAGGTTTCTGCTGCAAAAATCTGATTCCTGTGA 199
QY 337 GACA---CCCGTCCAGTAGATCTGGGCACCTTGGCCCAAGAAACAAAGAGTCTCCCTGAA 393
DB 200 CACAATTTCTCCCAACAAAGAGGACAAAGTGGTTATTGGCCAGAGAGTAGCCAGAG 259
QY 394 GAGCAGTGAATGGGTGAATCATTTGACAACTCTTTCCCATAGAGATGAGCTAGAG 453
DB 260 GAAGTCAAGAAATGGGCTGAATCCTGGAACCTGATAGTATGATGAAATGTTGGGTGCA 319
QY 454 GCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAAAAATATTGAAATTTTGATAGCC 513
DB 320 GCTTTCAAGCTTTCTTGAAGTCTGAATATAGTGAAGAGATATTGACTTCTGGATCAGC 379
QY 514 TGTGAAGATTTCAAGAAAGCAGGACCTCAACAATTCACCTTAAAGCAAGCAATA 573
DB 380 TGTGAAGATGACAGAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 439
QY 574 TATGAGAAATTTATACAGACTGATGCTCCCAAGAGGTTAACTTGAATTTTACACAAA 633
DB 440 TATAATGAATTCATCTCAGTCCAGGCAACCAAGAGGTGAACCTGGATTTTGCACAGG 499
QY 634 GAAGTCAATTAACAACAGCATCACTCAACCTCCACAGTTTTCAGTTTTCAGTCAAGAGC 693
DB 500 GAAGAGACAGCCGGAACATGCTAGAGCCCTACAATAACCTGCTTTGATGAGGCCAGAG 559

QY 694 AGAGTGTATCAGCTCATGGAACACAGACAGTGTATATACACGTTTCTGAAATCTGACATCTAT 753
DB 560 AAGATTTTCAACCTCATGGAAGAGTATCTTACCGCGCTTCTCTCAAGTCTCGATTTCTAT 619
QY 754 TTAGACTTGCAT 764
DB 620 CTTGATTGGT 630

RESULT 12
US-09-016-434-1290
; Sequence 1290, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith

CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1290:

SEQUENCE CHARACTERISTICS:

LENGTH: 1398 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: G299704

US-09-016-434-1290

Query Match 6.4%; Score 141.2; DB 4; Length 1398;

Best Local Similarity 62.7%; Pred. No. 3.8e-21;

Mismatches 237; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

QY 381 AGTCTCCCTGAGAGGCGAGTGAATGGGTGAATCATTTGACAAACTGCTTTCCCATAG 440
DB 278 ACTTTCTGCTGAAGTGAATGAATGGTCTCAATCTCTGGAATAACTTCTTGCAACCA 337
QY 441 AGATGGACTAGAGGCTTTTACCAGATTTCTTAAAACTGAATTCAGTGAAGAAAATATTGA 500
DB 338 AACTGGTCAAAATGCTTTTGAAGTTTCTTAAAGTCTGAATTCAGTGAAGAGATATTGA 397
QY 501 ATTTTGGATAGCCTGTGAAGATTTCAAGAAAGCAGGAGCCTCAACAAATTCACCTTAA 560
DB 398 GTTCTGGTGGCTGTGAAGACTATAAGAAAACAGAG---TCTGATCTTTTGGCCCTGTAA 454

QY 561 AGCAAAAGCAATATATACGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACTTGA 620
DB 455 AGCAGAGAGATATATAAGACATTTGTGCATTCAGATGCTGTGTAACAAATCAATATTGA 514
QY 621 TTTTTCACAAAAAGAGTTCATTACAAACAGCATCACTCAACCTTACCTCCACAGTTTGA 680
DB 515 CTTCCGCACTCGAGAATCTACAGCCAAAGAGATTAAAGCACCACACCCACCGTGTTTGA 574
QY 681 TGCTGCACAAAGCAGAGTGTATCAGCTCATCGGACAGACAGTATATACAGTTTCTGAA 740
DB 575 TGAAGCACAAAAAGTCTATATATCTTATATGGAAGAGGACTCTTATCCCGAGGTTCCTCAA 634
QY 741 ATCTGACATCTATTTAGA 758
DB 635 ATCAGATATTACTTAAA 652

RESULT 13

US-09-702-705-322

; Sequence 322, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 322

; LENGTH: 1398

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-702-705-322

Query Match 6.4%; Score 141.2; DB 4; Length 1398;

Best Local Similarity 62.7%; Pred. No. 3.8e-21;

Mismatches 237; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

QY 381 AGTCTCCCTGAGAGGCGAGTGAATGGGTGAATCATTTGACAAACTGCTTTCCCATAG 440
DB 278 ACTTTCTGCTGAAGTGAATGAATGGTCTCAATCTCTGGAATAACTTCTTGCAACCA 337
QY 441 AGATGGACTAGAGGCTTTTACCAGATTTCTTAAAACTGAATTCAGTGAAGAAAATATTGA 500
DB 338 AACTGGTCAAAATGCTTTTGAAGTTTCTTAAAGTCTGAATTCAGTGAAGAGATATTGA 397
QY 501 ATTTTGGATAGCCTGTGAAGATTTCAAGAAAGCAGGAGCCTCAACAAATTCACCTTAA 560
DB 398 GTTCTGGCTGGCTGTGAAGACTATAAGAAAACAGAG---TCTGATCTTTTGGCCCTGTAA 454
QY 561 AGCAAAAGCAATATATGAGAAATTTATACAGCTGATGCCCAAAAGAGGTTAACTTGA 620
DB 455 AGCAGAGAGATATATAAGCAATTTGTGCATTCAGATGCTGTGTAACAAATCAATATTGA 514
QY 621 TTTTTCACAAAAAGAGTTCATTACAAACAGCATCACTCAACCTTACCTCCACAGTTTGA 680
DB 515 CTTCCGCACTCGAGAATCTACAGCCAAAGAGATTAAAGCACCACACCCACCGTGTTTGA 574
QY 681 TGCTGCACAAAGCAGAGTGTATCAGCTCATCGGACAGACAGTATATACAGTTTCTGAA 740
DB 575 TGAAGCACAAAAAGTCTATATATCTTATGGAAGAGGACTCTTATCCCGAGGTTCCTCAA 634
QY 741 ATCTGACATCTATTTAGA 758

Db 635 ATCAGATATTACTTAAA 652

RESULT 14

US-09-736-457-322
; Sequence 322, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Lijun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 322
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-322

Query Match 6.4%; Score 141.2; DB 4; Length 1398;
Best Local Similarity 62.7%; Pred. No. 3.8e-21;
Matches 237; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

Qy 381 AGTCTCCCTGGAAGGAGGAGTGAATGGGGTGAATCAATTTGACAACTGCTTTCCCATAG 440
Db 278 ACTTCTGCTGCTGAAGTAAATGCAATGGTCTCAATCTCTGGAATACTTCTTGCAACCA 337
Qy 441 AGATGACTAGAGGCTTTTACAGATTCTTAAACTGAATTCAGTGAAGAAATATTGA 500
Db 338 AACTGGTCAAAATGCTTTGGAGTTTCTTAAAGTCTGAATTCAGTGAAGAAATATTGA 397
Qy 501 ATTTGGATAGCTGTGAAGATTTCAGAGAAAGGAGGAGCTCAACAAATTCACCTTAA 560
Db 398 GTTCTGGCTGGCTTGGAGACTATAAGAAACAGAG---TCTGATCTTTTGGCTGTAA 454
Qy 561 AGCAAAAGCAATATATAGAAATTTATACAGACTGATGCCCCCAAGAGGTTAACTTTGA 620
Db 455 AGCAGAAGAGATATATAAAGCAATTTGTGCAATTCAGATGCTGTAAACAAATCAATATTGA 514
Qy 621 TTTTCACAAAAGAGTCAATTAACAGAGTCACTCAACTACCTCCACAGTTTGA 680
Db 515 CTTCGGCACTCGAGATCTACAGCCAAAGAGATTAAAGCACCACCCACAGTTTGA 574
Qy 681 TGTGTCACAAAAGCAGAGTGTATCAGCTCATGGAACAAGACAGTTATACACGTTTCTGAA 740
Db 575 TGAAGCACAAAAGTCAATATATCTTATGAAAAGGACTCTTATCCAGGTTCTCTCAA 634
Qy 741 ATCTGACATCTATTAGA 758
Db 635 ATCAGATATTACTTAAA 652

RESULT 15

US-09-614-124B-322
; Sequence 322, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 322
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-124B-322

Query Match 6.4%; Score 141.2; DB 4; Length 1398;
Best Local Similarity 62.7%; Pred. No. 3.8e-21;
Matches 237; Conservative 0; Mismatches 138; Indels 3; Gaps 1;
Qy 381 AGTCTCCCTGGAAGGAGGAGTGAATGGGGTGAATTTGACAACTGCTTTCCCATAG 440
Db 278 ACTTCTGCTGCTGAAGTAAATGCAATGGTCTCAATCTCTGGAATACTTCTTGCAACCA 337
Qy 441 AGATGACTAGAGGCTTTTACAGATTCTTAAACTGAATTCAGTGAAGAAATATTGA 500
Db 338 AACTGGTCAAAATGCTTTGGAGTTTCTTAAAGTCTGAATTCAGTGAAGAAATATTGA 397
Qy 501 ATTTGGATAGCTGTGAAGATTTCAGAGAAAGGAGGAGCTCAACAAATTCACCTTAA 560
Db 398 GTTCTGGCTGGCTTGGAGACTATAAGAAACAGAG---TCTGATCTTTTGGCTGTAA 454
Qy 561 AGCAAAAGCAATATATAGAAATTTATACAGACTGATGCCCCCAAGAGGTTAACTTTGA 620
Db 455 AGCAGAAGAGATATATAAAGCAATTTGTGCAATTCAGATGCTGTAAACAAATCAATATTGA 514
Qy 621 TTTTCACAAAAGAGTCAATTAACAGAGTCACTCAACTACCTCCACAGTTTGA 680
Db 515 CTTCGGCACTCGAGATCTACAGCCAAAGAGATTAAAGCACCACCCACAGTTTGA 574
Qy 681 TGTGTCACAAAAGCAGAGTGTATCAGCTCATGGAACAAGACAGTTATACACGTTTCTGAA 740
Db 575 TGAAGCACAAAAGTCAATATATCTTATGAAAAGGACTCTTATCCAGGTTCTCTCAA 634
Qy 741 ATCTGACATCTATTAGA 758
Db 635 ATCAGATATTACTTAAA 652

Search completed: August 20, 2004, 12:36:24
Job time : 178.734 secs

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2004, 09:59:05 ; Search time 1035.39 Seconds
(without alignments)
10518.000 Million cell updates/sec

Title: US-09-894-749-1

Perfect score: 2217
Sequence: 1 gaattcggttcctactctaa.....aaaaaaaaagggcgccgc 2217

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3228839 seqs, 2456066551 residues

Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2217	100.0	2147	9	US-09-894-749-1
2	2041.6	92.1	2144	13	US-10-258-371B-19
3	1816.6	81.9	1884	17	US-10-115-635-133
4	1753.2	79.1	1840	13	US-10-258-371B-18
5	1448.2	65.3	1486	13	US-10-258-371B-6
6	782	35.3	848	9	US-09-867-550-847
7	596	26.9	1164	9	US-09-894-749-3
8	388	17.5	736	9	US-09-833-381-1010
9	227.2	10.2	241	13	US-10-258-371B-11
10	155.6	7.0	1345	13	US-10-342-867-839
11	155.6	7.0	1345	13	US-10-172-118-839
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13	155.6	7.0	1345	17	US-10-641-643-1243
14	155.6	7.0	1364	9	US-09-925-300-567

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15 155.6 7.0 1381 10 US-09-971-429B-32 Sequence 32, Appl
16 155.6 7.0 1382 10 US-09-971-392-13 Sequence 13, Appl
17 153.2 6.9 1744 9 US-09-206-639-2 Sequence 2, Appl
18 153.2 6.9 1923 15 US-10-411-224-55 Sequence 55, Appl
19 153.2 6.9 1923 16 US-10-047-021-55 Sequence 55, Appl
20 153.2 6.9 2076 13 US-10-240-425-345 Sequence 345, App
21 153.2 6.9 2190 17 US-10-641-643-795 Sequence 795, App
22 153.2 6.9 5809 15 US-10-133-013-103 Sequence 103, App
23 152.4 6.9 1629 12 US-10-152-319A-1995 Sequence 1995, App
24 152.4 6.9 1629 16 US-10-191-803-244 Sequence 244, App
25 145.2 6.5 543 15 US-10-398-953-2 Sequence 2, Appl
26 145.2 6.5 817 15 US-10-398-953-6 Sequence 6, Appl
27 144.8 6.5 1283 10 US-09-814-353-19578 Sequence 19578, A
28 143.8 6.5 1800 16 US-10-305-720-1091 Sequence 1091, App
29 143.8 6.5 1531 15 US-10-198-846-9863 Sequence 9863, App
30 143.8 6.5 1869 15 US-10-175-523-144 Sequence 144, App
31 143.8 6.5 2752 15 US-10-198-846-13843 Sequence 13843, A
32 143.8 6.5 2934 10 US-09-939-209A-1 Sequence 1, Appl
33 143.8 6.5 3165 14 US-10-044-090-113 Sequence 113, App
34 143.8 6.5 3167 10 US-09-918-624B-6 Sequence 6, Appl
35 141.2 6.4 1329 15 US-10-247-671-107 Sequence 107, App
36 141.2 6.4 1380 9 US-09-925-301-450 Sequence 450, App
37 141.2 6.4 1398 9 US-09-736-457-322 Sequence 322, App
38 141.2 6.4 1398 9 US-09-902-941-322 Sequence 322, App
39 141.2 6.4 1398 9 US-09-849-626-322 Sequence 322, App
40 141.2 6.4 1398 10 US-09-476-300-322 Sequence 322, App
41 141.2 6.4 1398 10 US-09-960-705-870 Sequence 870, App
42 141.2 6.4 1398 10 US-09-873-319-567 Sequence 567, App
43 141.2 6.4 1398 13 US-10-283-017-322 Sequence 322, App
44 141.2 6.4 1398 15 US-10-017-754-322 Sequence 322, App
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ALIGNMENTS

RESULT 1

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US-09-894-749-1
; Sequence 1, Application US/09894749
; Patent No. US20020081683A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/894,749
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/244,314
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2217
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)..(867)
US-09-894-749-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Allison

/ APPLICANT: MURRAY, David L
/ TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
/ FILE OF INVENTION: RGS18, AND USES THEREOF
/ FILE REFERENCE: A3656 US PCT
/ CURRENT APPLICATION NUMBER: US/10/258,371B
/ CURRENT FILING DATE: 2003-06-04
/ PRIOR APPLICATION NUMBER: GB001883.334
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: US60/200,786
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 19
/ LENGTH: 2144
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-258-371B-19

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DB	2103	TTATCT	GACAATAAAAGCTCTGACTGAA	2130
RESULT 3				
US-10-115-635-133				
; Sequence 133, Application US/10115635				
; Publication No. US20040137434A1				
; GENERAL INFORMATION:				
; APPLICANT: Tang, Y. Tom				
; APPLICANT: Zhou, Ping				
; APPLICANT: Goodrich, Ryle				
; APPLICANT: Liu, Chenghua				
; APPLICANT: Asundi, Vinod				
; APPLICANT: Ren, Feiyan				
; APPLICANT: Zhang, Jie				
; APPLICANT: Zhao, Qing A.				
; APPLICANT: Xue, Aidong J.				
; APPLICANT: Yang, Yongshong				
; APPLICANT: Wehrman, Tom				
; APPLICANT: Drmanac, Radcoje T.				
; TITLE OF INVENTION: Novel Nucleic Acids and				
; TITLE OF INVENTION: Polypeptides				
; FILE REFERENCE: 797CON				
; CURRENT APPLICATION NUMBER: US/10/115,635				
; CURRENT FILING DATE: 2002-04-03				
; PRIOR FILING DATE: 2000-11-17				
; NUMBER OF SEQ ID NOS: 362				
; SOFTWARE: pt FL_genes Version 2.0				
; SEQ ID NO 133				
; LENGTH: 1884				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (157)..(864)				
US-10-115-635-133				
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Best Local Similarity 99.9%; Pred. No. 0;				
Matches 182; Conservative 0; Mismatches 0; Indels 1; Gaps 1;				
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DB	178	TTTTCTCAAA	TAAATATGTGTGAATCAAAAGAAAAAACTTTTTTCAAGTTAATACATGGT	237
QY	241	TCAGAAAA	AGAAAGAAACAAAGCAAGAGACCCAAAATCAGAGCTAGGAAAGAAAGTAAGA	300
DB	238	TCAGAAAA	AGAAAGAAACAAAGCAAGAGACCCAAAATCAGAGCTAGGAAAGAAAGTAAGA	297
QY	301	CTAAGTCT	CTTGTGCAGAAACCTTGAGTTTTCATGAAGACACCCCGCTCCAGTAGATCTGGG	360

QY 1321 AATAGTGTAGAGTGTATCTGGTTCTTACAAATGGGAGATGACAGAAATTTATTTGGTT 1380
 Db 1324 AATAGTGTAGAGTGTATCTGGTTCTTACAAATGGGAGATGACAGAAATTTATTTGGTT 1383
 QY 1381 ACTACTAACCCCTGTCACCAAGATAGTAATATATACCTCTAGTTATAGCCAGCAACAGGAA 1440
 Db 1384 ACTACTAACCCCTGTCACCAAGATAGTAATATATACCTCTAGTTATAGCCAGCAACAGGAA 1443
 QY 1441 CTTTGTGAGAGACATTTCTCTACAGAACTTCAGATTAATATATATATATATATATATATG 1500
 Db 1444 CTTTGTGAGAGACATTTCTCTACAGAACTTCAGATTAATATATATATATATATATATATG 1503
 QY 1501 ACTGAGAAATAGATCCACATTTTGAATCTATCTTAAGTGAACATGAGCTACCCAGTTAT 1560
 Db 1504 ACTGAGAAATAGATCCACATTTTGAATCTATCTTAAGTGAACATGAGCTACCCAGTTAT 1563
 QY 1561 ACAAGTACTTCTGTGTGTGTCACAGAAACATGACCAAGATTTTGCATATCTCCAGGTAGGGA 1620
 Db 1564 ACAAGTACTTCTGTGTGTGTCACAGAAACATGACCAAGATTTTGCATATCTCCAGGTAGGGA 1623
 QY 1621 ACTAGTACTACTCTTATACCGGCTAAGAAACCTTGCTACTAACTATTAGGCCATCA 1680
 Db 1624 ACTAGTACTACTCTTATACCGGCTAAGAAACCTTGCTACTAACTATTAGGCCATCA 1683
 QY 1681 ATGGCTTGAATAAAAACCCAGAGAGGTTTTCACAGGACGTCTCATGTTTGGCCCTTTAG 1740
 Db 1684 ATGGCTTGAATAAAAACCCAGAA-GTTTTTCCAGGACGCTCATGTTTGGCCCTTTAG 1742
 QY 1741 AATTGGGTAGAAATCAGAAATGAGATGAGGAGAGAGAGGAGTCTTAGGCCCTAGC 1800
 Db 1743 AATTGGGTAGAAATCAGAAATGAGATGAGGAGAGAGAGGAGTCTTAGGCCCTAGC 1802
 QY 1801 GATTTGGGCATCTGCCACATTTGTTTCATATTCAGAAAG 1838
 Db 1803 GATTTGGGCATCTGCCACATTTGTTTCATATTCAGAAAG 1840
 RESULT 5
 US-10-258-371B-6
 ; Sequence 6, Application US/10258371B
 ; Publication No. US20040067903A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS-GAGNON, Alison
 ; APPLICANT: MURRAY, David L
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
 ; TITLE OF INVENTION: RGS18, AND USES THEREOF
 ; FILE REFERENCE: A3656 US PCT
 ; CURRENT APPLICATION NUMBER: US/10/258,371B
 ; CURRENT FILING DATE: 2003-06-04
 ; PRIOR APPLICATION NUMBER: GB001883.334
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: US60/206,786
 ; PRIOR FILING DATE: 2000-04-28
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6
 ; LENGTH: 1486
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-258-371B-6
 Query Match 65.3%; Score 1448.2; DB 13; Length 1486;
 Best Local Similarity 99.4%; Pred. No. 8,1e-274;
 Matches 1464; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
 QY 656 CTCACCTACCTCCACAGTTTGTGTGTCACAAAGCAGAGTGTATCAGTCTATGGAAC 715
 Db 1 CTCACCTACCTCCACAGTTTGTGTGTCACAAAGCAGAGTGTATCAGTCTATGGAAC 60
 QY 716 AAGACAGTATACAGTTTCTGAATCTGACATCTATTAGACTTTGATGGAAGGAGAC 775
 Db 61 AAGACAGTATACAGTTTCTGAATCTGACATCTATTAGACTTTGATGGAAGGAGAC 120

776 CTCAGAGACCAACAAATCTTAGGAGAGATCAGCTCATTTTACCTGCAATGAATTTCCAAG 835
 Db 121 CTCAGAGACCAACAAATCTTAGGAGAGATCAGCTCATTTTACCTGCAATGAATTTCCAAG 180
 QY 836 ATCTACAATCAGATGTTGCCATTTGGTTATAAAGAAAAATGATTTTGGCTCATTTTATGA 895
 Db 181 ATCTACAATCAGATGTTGCCATTTGGTTATAAAGAAAAATGATTTTGGCTCATTTTATGA 240
 QY 896 CAATCTATACATCTGCTTCTTAACATATCGATGTTTAAAGATTTGGTCCCATCT 955
 Db 241 CAATCTATACATCTGCTTCTTAACATATCGATGTTTAAAGATTTGGTCCCATCT 300
 QY 956 TTAATCTGAATATATGCTGTAATTTTAAAAATCTAAAAACAAACCTTTCTGCTA 1015
 Db 301 TTAATCTGAATATATGCTGTAATTTTAAAAATCTAAAAACAAACCTTTCTGCTA 360
 QY 1016 ACAATATACATCAGATCTGCCAGTATATCTGTAACACCTTCTATTGATGTCATCC 1075
 Db 361 ACAATATACATCAGATCTGCCAGTATATCTGTAACACCTTCTATTGATGTCATCC 420
 QY 1076 ATTATATAATCAGAAAAAAACCTTATTTCTTAATCAAAAGCAGTACAAAAAAGTAATAA 1135
 Db 421 ATTATATAATCAGAAAAAAACCTTATTTCTTAATCAAAAGCAGTACAAAAAAGTAATAA 480
 QY 1136 TGTATTATAGATGTAGAGTTAAGTAAGTTTAAAGTTTTCGAAAGTTGTCAAAAAGTTC 1195
 Db 481 TGTATTATAGATGTAGAGTTAAGTAAGTTTAAAGTTTTCGAAAGTTGTCAAAAAGTTC 540
 QY 1196 AAACAAAGTCTAGTTGGGATTTTACCAAGCAGCATAATATGTTTATATAAACATA 1255
 Db 541 AAACAAAGTCTAGTTGGGATTTTACCAAGCAGCATAATATGTTTATATAAACATA 600
 QY 1256 ATAATCTCAGATATCCAAATGTTTCCAGATGAGATTTTCCAAATGAATGTTCTTTT 1315
 Db 601 ATAATCTCAGATATCCAAATGTTTCCAGATGAGATTTTCCAAATGAATGTTCTTTT 660
 QY 1316 TTGGTAATAGTGTAGAGTGTCTGTTCTTCAATGGGAGATGAGACATTTATTAT 1375
 Db 661 TTGGTAATAGTGTAGAGTGTCTGTTCTTCAATGGGAGATGAGACATTTATTAT 720
 QY 1376 GGGTTACTACTAACCTGTCCCAAGATAGTAATATCACCTCTAGTTATAGCCAGCAAC 1435
 Db 721 GGGTTACTACTAACCTGTCCCAAGATAGTAATATCACCTCTAGTTATAGCCAGCAAC 780
 QY 1436 AGGAATTTTGTGAAGACATCTCTCAGAGACTTCAGATTAATATATCTAGAT 1495
 Db 781 AGGAATTTTGTGAAGACATCTCTCAGAGACTTCAGATTAATATATCTAGAT 840
 QY 1496 TAATGACTGAGATAAGATCCACATTTGAACCTATTCCCTAAGTGAACATGGACGTACCCA 1555
 Db 841 TAATGACTGAGATAAGATCCACATTTGAACCTATTCCCTAAGTGAACATGGACGTACCCA 900
 QY 1556 GTTATCAAAAGTACTTCTGTTGTGTACAGAAACATGACAGATTTTGCATATCTCAGGT 1615
 Db 901 GTTATCAAAAGTACTTCTGTTGTGTACAGAAACATGACAGATTTTGCATATCTCAGGT 960
 QY 1616 AGGGAATAGTAGACTCTTATCACCGGCTAAGAAAACTTGTCTACTATAATATTAGGC 1675
 Db 961 AGGGAATAGTAGACTCTTATCACCGGCTAAGAAAACTTGTCTACTATAATATTAGGC 1020
 QY 1676 CATCAATGGCTTGAATAAAAACCCAGAGAGTTTTCAGAGACGTCTCATGTTGGGCC 1735
 Db 1021 CATCAATGGCTTGAATAAAAACCCAGAGAG-GTTTTTCCAGGACGTCTCATGTTGGGCC 1079
 QY 1736 TTTAGAAATGGGTGAAATCAGAAATGAGATGAGGGAAGCAAGAGGCTTAGGCC 1795
 Db 1080 TTTAGAAATGGGTGAAATCAGAAATGAGATGAGGGAAGCAAGAGGCTTAGGCC 1139
 QY 1796 CTAGCAGTTTGGGCATCTGCCACATTTGGTTTCATATTAGAAAGTGTATCTCATTGATTA 1855
 Db 1140 CTAGCAGTTTGGGCATCTGCCACATTTGGTTTCATATTAGAAAGTGTATCTCATTGATTA 1199


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QY 187 CAATAAATATCTGTCAATCAAAAGAAAGAACTTTTTCAGTAAATCAATCATGGTTCAGGA 246
DB 161 CAATTAATATCTGTCAATCAAAAGAAAGAACTTTTTCAGTAAATCAATCATGGTTCAGGA 220
QY 247 AAAGAAGAAACCAAGCAAGAAAGCAAAATTCAGAGCTAAAGGAAAGAAAGAAATAGACTAAGT 306
DB 221 AAAGAAGAAACCAAGCAATCGAGGCCAAATTCAGAGCGAAAGAAAGAAAGAAATAGACTAAGT 280
QY 307 CTTCTTGTGCGAAACCTGAGTTTCATGAAGCACCCGCTCCAGTAGATCTGGGCACTTG 366
DB 281 CTTCTCTACAGAGCCTGACTTCCATGGAGAGACTCAAGCCAGTAGATCTGGCCCTCTTG 340
QY 367 GCGAAAGAAACCAAGAGTCTCCCTCAAGAGGAGGAGTGAATGGGGTGAATCTTTGACAAA 426
DB 341 GCGAAAGAAACCAAGAGTCTCTCTGAAGNAGCAGTGAATGGGCTGAATCTTTGACAAA 400
QY 427 CTGCTTCCATAGAGATGGAAGTAGAGGCTTTTACAGATTTTCAAGATTTCTTAAACTGAATTCAGT 486
DB 401 TTGCTCTCTATAGAGATGGAGTGGATGCTTTTACAGATTTTCTTAAACTGAATTCAGT 460
QY 487 GAAGAAATATTTGAATTTTGGATAGCCTGTGAGAGTTTCAAGAAAGCAAGGACCTCAA 546
DB 461 GAGGAGAACTTTGAATTTTGGTCTGCTCTGAAGNAGCAGTGAATGGGCTGAATCTTTGACAAA 520
QY 547 CAAATTCACCTTAAAGCAAAAGCAATATATATGAGAAATTTTACAGACTGATGCCCAAAA 606
DB 521 CAAATCATCTTAAAGCAAAAGCAATCTATGAGAAATTCATTCAGAAATGATGCCCAAAA 580
QY 607 GAGGTAACTTTGATTTTACACAAAGNAGTCATCAACACAGCATCACTCAACCTACC 666
DB 581 GAGGTAACTTTGATTTTCTACTAAGAGAAATTTGCTTAAGAGCATCGCCAGCCCACT 640
QY 667 CTCACAGTTTTGATGCTGCACAAAGCAGAGTGTATCAGCTCATCGGAAACAAAGACAGTTAT 726
DB 641 CTCACAGTTTTGATGCGCACAAAGCAGAGTGTATCAGCTCATCGGAAACATGACAGTTAT 700
QY 727 ACAGTTTTCTGAAATCTGACATCTATTTAGACTTGTGGAAGNAGACCTCAGAGACCA 786
DB 701 AAACGCTTTTGAATCTGAGACCTACTTACATTTGTATAGAGGAAGACCTCAGAGACCA 760
QY 787 ACAATCTTTAGAGAGGATCAGCTCATTTTCAATGCAATGATTCGAAGATGTAACAATCA 846
DB 761 ACAACCTTTAGAGAGGATCAGCATCTATTTACTTACATGATTTTCAAGATGTAAGATCA 820
QY 847 GATGTGCCATTTGGTTATPAAAGAAATTTGATTTTGGCTCATTTTATGACAAATTTATAC 906
DB 821 GATGTGCCATTTGGTTATGATPAAAGATTCATTTGCTCTCTTTTGAATGATGTATGTAT 880
QY 907 ATC-----TGCTTCAACATATCGCATGTTTATGTTAAGA 941
DB 881 ATCTAAATATATATACTAATACTAATGTGACTTCTTAAATATAGTGTGTATGATPAAAGA 940
QY 942 TTGTGCTCCATCTTTAAACTGAAATATGTCATGTGAAATTTATTTTAAATAATGTAATAAC 1001
DB 941 GATGATTTTCAATTT-----TAAATACACCATGCAAAATACATATTAATGTAAGAACTT 994
QY 1002 AAACTTTCTGTAACAAATACATACAGTATCTGCCAGTATATCTGTAACAACTTCTA 1061
DB 995 TTTATATTATATACTAAATAATTCATCATCTATCTCCGAAATATTTTATGAAATCTATC 1054
QY 1062 TTTGATGTCTATTCCTATTTATATATC 1085
DB 1055 TGATATCTCTATTTCTAATAAATTC 1078
```

RESULT 8

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US-09-833-381-1010
; Sequence 1010, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
```

```
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1010
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(736)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1010
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Query Match 17.5%; Score 388; DB 9; Length 736;

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Best Local Similarity 100.0%; Pred. No. 4.2e-66;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 481 TTCAGTGAAGAAATATTCGAATTTTGGATAGCCTGTGAAGATTTTCAAGAAAGCAAGGCA 540
DB 4 TTCAGTGAAGAAATATTCGAATTTTGGATAGCCTGTGAAGATTTTCAAGAAAGCAAGGCA 63
QY 541 CCTCAACAATTCACCTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCC 600
DB 64 CCTCAACAATTCACCTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCC 123
QY 601 CCAAAAGAGTTTAACTTGTATTTTTCACAAAGAAAGTCAATTCACAAAGCAGCTCACTCAA 660
DB 124 CCAAAAGAGTTTAACTTGTATTTTTCACAAAGAAAGTCAATTCACAAAGCAGCTCACTCAA 183
QY 661 CCTACCTCCACAGTTTTCATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAGAC 720
DB 184 CCTACCTCCACAGTTTTCATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAGAC 243
QY 721 AGTTATACAGTTTTCGTAATCTGACATCTATTTAGACTTGTATGGAAGAGACCTCAG 780
DB 244 AGTTATACAGTTTTCGTAATCTGACATCTATTTAGACTTGTATGGAAGAGACCTCAG 303
QY 781 AGACCAACAATCTTAGGAGACGATCACGCTCATTTTACCTGCAATGAATTCGAAGATGTA 840
DB 304 AGACCAACAATCTTAGGAGACGATCACGCTCATTTTACCTGCAATGAATTCGAAGATGTA 363
QY 841 CAATCAGATGTTGCCATTTGGTTATAAA 868
DB 364 CAATCAGATGTTGCCATTTGGTTATAAA 391
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RESULT 9

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US-10-258-371B-11
; Sequence 11, Application US/10258371B
; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Alison
; APPLICANT: MURRAY, David L
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
; FILE REFERENCE: A3656 US PCT
; CURRENT APPLICATION NUMBER: US/10/258,371B
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: GB001883.334
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/200,786
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-258-371B-11
```

Query Match 10.2%; Score 227.2; DB 13; Length 241;
Best Local Similarity 96.7%; Pred. No. 8.2e-35;
Matches 232; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 487 GAAGAAATATTGAATTTGGATAGCCCTGTGAAGATTTCAAGAAAGCAAGGGACCTCAA 546
DB 1 GAGGAAATCTGGAGTTCTGGATAGCCCTGTGAAGATTTCAAGAAAGCAAGGGACCTCAA 60

QY 547 CAATTCACCTTAAGCAAGCAATATATAGAAATTTATACAGACTGTATGCCCAAAA 606
DB 61 CAATTCACCTTAAGCAAGCAATATATAGAAATTTATACAGACTGTATGCCCAAAA 120

QY 607 GAGGTAAACCTTTGATTTTACACAAAAGAGTCAATTAACAACAGCATCAACCTACC 666
DB 121 GAGGTAAACCTTTGATTTTACACAAAAGAGTCAATTAACAACAGCATCAACCTACC 180

QY 667 CTCACAGTTTGTGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAAGACAGTTAT 726
DB 181 CTCACAGTTTGTGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAAGCAGAGTTAT 240

RESULT 10

US-10-342-887-839
; Sequence 839, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mac, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 839
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_002923
; DATABASE ENTRY DATE: 2001-06-18
US-10-342-887-839

Query Match 7.0%; Score 155.6; DB 13; Length 1345;
Best Local Similarity 63.2%; Pred. No. 2.1e-20;
Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 385 TCCCTGAGAGCGAGTGAATGGGTGAATCATTTTGACAACTGCTTTCCCATAGAT 444
DB 249 TCTCTGAGAGCGAGTGTGTCAGAAAGCATTTTGAGAGTCTGTAGCCAGCAATAT 308

QY 445 GGACTAGAGGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAAAATATTGAATTT 504
DB 309 GGTCTGTGCTGATTCAGGGCTTTTAAAGTCGGAATTTCTGTGAAGAAAATATTGAATTC 368

QY 505 TGATAGCCTGTGAAGATTTCAAGAAAGCAAGGACCTCAACAAATTCACCTTAAGCA 564
DB 369 TGGTGGCCCTGTGAAGACTTCAAAAACCAATCACCCCAAGAGCTGTCTCTCAAAAGCA 428

QY 565 AAAGCAATATATGAGAAATTTATACAGACTGTATGCCCAAAAGAGGTTAACTTCATTTT 624
DB 429 AGGAAATATATATCTGACTTCATAGAAAGAGAGCTCCAAAGAGATAAATAGATTTT 488

QY 625 CACACAAAAGAGTCAATTAACAACAGCATCACTCAACCTCCACCTTCAGTTTGTGCT 684
DB 489 CAAACCAAACTCTGATTTGCCAGATATACAAAGAGCTACAAAGTGGCTGCTTTTACAACT 548

QY 585 GCACAAAGCAGTGTATCAGCTCATGGAACAAGACAGTTATACACCTTTTCTGAAATCT 744
DB 549 GCCCAGAAAAGGGTATACAGTTGATGGAGAACAACTCTTATCTCTCTCTTCTGGAGTCA 608

QY 745 GACATCTATTAGACTTG 762
DB 609 GAATTTCTACCAGGACTTG 626

DB 489 CAAACCAAACTCTGATTTGCCAGATATATACAAAGAGCTACAAAGTGGCTGCTTTTACAACT 548
QY 585 GCACAAAGCAGTGTATCAGCTCATGGAACAAGACAGTTATACACCTTTTCTGAAATCT 744
DB 549 GCCCAGAAAAGGGTATACAGTTGATGGAGAACAACTCTTATCTCTCTCTTCTGGAGTCA 608

QY 745 GACATCTATTAGACTTG 762
DB 609 GAATTTCTACCAGGACTTG 626

RESULT 11

US-10-172-118-839
; Sequence 839, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mac, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 839
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_002923
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-839

Query Match 7.0%; Score 155.6; DB 13; Length 1345;
Best Local Similarity 63.2%; Pred. No. 2.1e-20;
Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 385 TCCCTGAGAGCGAGTGAATGGGTGAATCATTTTGACAACTGCTTTCCCATAGAT 444
DB 249 TCTCTGAGAGCGAGTGTGTCAGAAAGCATTTTGAGAGTCTGTAGCCAGCAATAT 308

QY 445 GGACTAGAGGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAAAATATTGAATTT 504
DB 309 GGTCTGTGCTGATTCAGGGCTTTTAAAGTCGGAATTTCTGTGAAGAAAATATTGAATTC 368

QY 505 TGATAGCCTGTGAAGATTTCAAGAAAGCAAGGACCTCAACAAATTCACCTTAAGCA 564
DB 369 TGGTGGCCCTGTGAAGACTTCAAAAACCAATCACCCCAAGAGCTGTCTCTCAAAAGCA 428

QY 565 AAAGCAATATATGAGAAATTTATACAGACTGTATGCCCAAAAGAGGTTAACTTCATTTT 624
DB 429 AGGAAATATATATCTGACTTCATAGAAAGAGAGCTCCAAAGAGATAAATAGATTTT 488

QY 625 CACACAAAAGAGTCAATTAACAACAGCATCACTCAACCTCCACCTTCAGTTTGTGCT 684
DB 489 CAAACCAAACTCTGATTTGCCAGATATACAAAGAGCTACAAAGTGGCTGCTTTTACAACT 548

QY 585 GCACAAAGCAGTGTATCAGCTCATGGAACAAGACAGTTATACACCTTTTCTGAAATCT 744
DB 549 GCCCAGAAAAGGGTATACAGTTGATGGAGAACAACTCTTATCTCTCTCTTCTGGAGTCA 608

QY 745 GACATCTATTAGACTTG 762
DB 609 GAATTTCTACCAGGACTTG 626

RESULT 12

US-10-305-720-1278
 ; Sequence 1278, Application US/10305720
 ; Publication No. US20040010136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
 ; FILE REFERENCE: PA-0002-1 CON
 ; CURRENT APPLICATION NUMBER: US/10/305,720
 ; CURRENT FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: 09/016,434
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 1490
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1278
 ; LENGTH: 1345
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: GenBank ID No. US20040010136A1 g292054
 ; US-10-305-720-1278

Query Match 7.0%; Score 155.6; DB 16; Length 1345;
 Best Local Similarity 63.2%; Pred. No. 2.1e-20;
 Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY	385	TCCCTGGAAGAGCAGTGAATGGGTGAATCATTTGACAAACTGCTTTCCCATAGAGAT	444
Db	249	TCTCTGAGAGAGCAGCTGGTTCAGAGCATTTGACGAGCTCTAGCCAGCAAAATAT	308
QY	445	GGACTAGAGCGCTTTACAGATTTCTTAAACTGATTCAGTGAAGAAATATTGAATTT	504
Db	309	GGTCTGTGCTGCTTACAGATTTCTTAAAGTCGGAATTTCTGTGAAGAAATATTGAATTC	368
QY	505	TGATAGCTGTGAGATTTCAAGAAAGCAGGACCTCAACAAATTCACCTTAAAGCA	564
Db	369	TGCTGGCTGTGAGATTTCAAGAAAGCAGGACCTCAACAAATTCACCTTAAAGCA	428
QY	565	AAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACCTTGATTTT	624
Db	429	AGGAAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACCTTGATTTT	488
QY	625	CACACAAAAGAGTCAATTAACAACAGCATCACTCAACCTACCTCCACAGTTTGTATGCT	684
Db	489	CAACCAAACTCTGATTTGCCAGATATACAAGAGCTACAAGTGGTCTTCAACT	548
QY	745	GACATCTATTGACTTG 762	
Db	609	GAATTCACAGGACTTG 626	

RESULT 13

US-10-641-643-1243
 ; Sequence 1243, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; Jeffrey J. Seilhamer
 ; Susan G. Stuart
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA

COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/641,643
 FILING DATE: 14-Aug-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1243:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1345 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g292054
 SEQUENCE DESCRIPTION: SEQ ID NO: 1243 :
 US-10-641-643-1243

Query Match 7.0%; Score 155.6; DB 17; Length 1345;
 Best Local Similarity 63.2%; Pred. No. 2.1e-20;
 Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY	385	TCCCTGGAAGAGCAGTGAATGGGTGAATCATTTGACAAACTGCTTTCCCATAGAGAT	444
Db	249	TCTCTGAGAGAGCAGCTGGTTCAGAGCATTTGACGAGCTCTAGCCAGCAAAATAT	308
QY	445	GGACTAGAGCGCTTTACAGATTTCTTAAACTGATTCAGTGAAGAAATATTGAATTT	504
Db	309	GGTCTGTGCTGCTTACAGATTTCTTAAAGTCGGAATTTCTGTGAAGAAATATTGAATTC	368
QY	505	TGATAGCTGTGAGATTTCAAGAAAGCAGGACCTCAACAAATTCACCTTAAAGCA	564
Db	369	TGCTGGCTGTGAGATTTCAAGAAAGCAGGACCTCAACAAATTCACCTTAAAGCA	428
QY	565	AAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACCTTGATTTT	624
Db	429	AGGAAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACCTTGATTTT	488
QY	625	CACACAAAAGAGTCAATTAACAACAGCATCACTCAACCTACCTCCACAGTTTGTATGCT	684
Db	489	CAACCAAACTCTGATTTGCCAGATATACAAGAGCTACAAGTGGTCTTCAACT	548
QY	745	GACATCTATTGACTTG 762	
Db	609	GAATTCACAGGACTTG 626	

RESULT 14

US-09-925-300-567
 ; Sequence 567, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05988

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1993-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 567

; LENGTH: 1364

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1362)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-300-567

Query Match 7.0%; Score 155.6; DB 9; Length 1364;

Best Local Similarity 63.2%; Pred. No. 2.1e-20;

Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 385 TCCCTGAAGGCGAGTGAATGGGTGAATCATTTGACAAACTGCTTTCCCATAGAGAT 444

Db 246 TCTCCTGAGGAAGCACAGCTGTGGTCAGAGCATTGTGACGCTCTAGCCAGCAATAT 305

QY 445 GGACTAGAGGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAAATATTGAATTT 504

Db 306 GGTCTTGTGCAATCAGGCGCTTTTAAAGTCGGAATTCGTGAAGAAATATTGAATTC 365

QY 505 TGGATAGGCTGTGAAGATTTCAAGAAAAGCAAGGAGCCTCAACAAATTCACCTTAAAGCA 564

Db 366 TGGCTGGCTGTGAAGACTTCBAAAAACCAATCACCCTCAAGCTCTCTCAAAAGCA 425

QY 565 AAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACTTGATTTT 624

Db 426 AGGAAATATATACCTGACTTTCATGAAAAGGAAAGCTCCAAAAGAGATTAACATAGATTT 485

QY 625 CACACAAAAGAGTCAATACAAACAGCATCACTCAACTACCTCCACAGTTTGTGCT 684

Db 486 CAAACCAAACTCTGATTTGCCAGATATACAGAGCTCAAGTGGCTGCTTTACAACT 545

QY 685 GCACAAAGCAGAGTGTATCAGCTCATGGAACAAGACAGTTATACACGTTTTCTGAAATCT 744

Db 546 GCCCAGAAAAGGATATACAGCTTGTATGAGAACAACTCTTATCTCTGTTTTCTTGGAGTCA 605

QY 745 GACATCTATTAGACTTG 762

Db 606 GAATTCACAGGACTTG 623

RESULT 15

US-09-971-429B-32

; Sequence 32, Application US/09971429B

; Publication No. US20030175704A1

; GENERAL INFORMATION:

; APPLICANT: LaseX, Amy K. W.

; APPLICANT: Shyjan, Andrew W.

; APPLICANT: Turner, Christopher M.

; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER

; FILE REFERENCE: PA-0040 US

; CURRENT APPLICATION NUMBER: US/09/971,429B

; CURRENT FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: 60/239,024

; PRIOR FILING DATE: 2000-04-10

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: PERL Program

; SEQ ID NO 32

; LENGTH: 1381

; TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20030175704A1 989992.12

US-09-971-429B-32

Query Match 7.0%; Score 155.6; DB 10; Length 1381;

Best Local Similarity 63.2%; Pred. No. 2.1e-20;

Matches 239; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 385 TCCCTGAAGGCGAGTGAATGGGTGAATCATTTGACAAACTGCTTTCCCATAGAGAT 444

Db 262 TCTCCTGAGGAAGCACAGCTGTGGTCAGAGCATTGTGACGCTCTAGCCAGCAATAT 321

QY 445 GGACTAGAGGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAAATATTGAATTT 504

Db 322 GGTCTTGTGCAATCAGGCGCTTTTAAAGTCGGAATTCGTGAAGAAATATTGAATTC 381

QY 505 TGGATAGGCTGTGAAGATTTCAAGAAAAGCAAGGAGCCTCAACAAATTCACCTTAAAGCA 564

Db 382 TGGCTGGCTGTGAAGACTTCBAAAAACCAATCACCCTCAAGCTCTCTCAAAAGCA 441

QY 565 AAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAAAGAGGTTAACTTGATTTT 624

Db 442 AGGAAATATATATCTGACTTTCATGAAAAGGAAAGCTCCAAAAGAGATTAACATAGATTT 501

QY 625 CACACAAAAGAGTCAATACAAACAGCATCACTCAACTACCTCCACAGTTTGTGCT 684

Db 502 CAAACCAAACTCTGATTTGCCAGATATACAGAGCTCAAGTGGCTGCTTTACAACT 561

QY 685 GCACAAAGCAGAGTGTATCAGCTCATGGAACAAGACAGTTATACACGTTTTCTGAAATCT 744

Db 562 GCCCAGAAAAGGATATACAGCTTGTATGAGAACAACTCTTATCTCTGTTTTCTTGGAGTCA 621

QY 745 GACATCTATTAGACTTG 762

Db 622 GAATTCACAGGACTTG 639

Search completed: August 20, 2004, 16:40:45

Job time : 1038.39 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2004, 05:11:40 ; Search time 6012.98 Seconds
(without alignments)
11010.254 Million cell updates/sec

Title: US-09-894-749-1

Perfect score: 2217
Sequence: 1 gaattcgcttcacatcctaa.....aaaaaaaaagggcgccgc 2217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vit.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gsl.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	998.2	45.0	1201	9	AL579846
c 2	918.2	41.4	1201	9	AL557903
c 3	872.2	39.3	923	13	BX349093
c 4	688.2	31.0	921	13	BX350311

5	680.4	30.7	703	14	CD642093
6	655	29.5	708	29	AY420372
7	643	29.0	655	12	BG572311
8	611	27.5	810	12	BG564257
9	596	26.9	1860	11	AK036407
10	568	25.6	705	9	AV714060
11	565.4	25.5	639	9	AV716055
12	564.2	25.4	626	9	AV714044
13	557.6	25.2	723	14	CF181629
14	550	24.8	661	14	CD466872
15	537	24.2	537	28	AQ317367
16	535.6	24.2	625	9	AV715708
17	519.8	23.4	652	14	CB553797
18	511.8	23.1	764	14	CD468328
19	507.6	22.9	697	12	BG253969
20	499.4	22.5	789	14	CD468976
21	486.8	22.0	701	9	AV712845
22	485.2	21.0	589	29	AY420373
23	449.6	20.3	655	29	AY420374
24	441.6	19.9	448	28	AQ053459
25	419.6	18.9	538	13	BU698389
26	417.2	18.8	716	14	CD465070
27	409	18.4	411	9	AA195206
28	404	18.2	431	28	AQ887601
29	395.8	17.9	473	14	W04905
30	380.6	17.2	409	12	BM145481
31	380.2	17.1	700	13	BY750625
32	370	16.7	484	14	N98410
33	352.8	15.9	861	14	CF257072
34	348.6	15.7	618	13	BY722727
35	345.2	15.6	666	10	BB660526
36	334.4	15.1	472	14	N69945
37	322	14.5	772	13	BU285628
38	306.4	13.8	616	10	BB629298
39	281.6	12.7	739	12	BI909559
40	279.2	12.6	781	13	BU361362
41	278.4	12.6	370	12	BM146419
42	277.6	12.5	674	14	CD465007
43	276	12.4	276	14	NS9342
44	273.6	12.3	706	14	CD468899
45	272.4	12.3	599	12	BG625427

ALIGNMENTS

RESULT 1
AL579846/c
LOCUS
DEFINITION AL579846 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ003YJ10 3-PRIME, mRNA sequence.
ACCESSION AL579846
VERSION AL579846.2 GI:31318126
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12945287.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 131 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 261.f For more information about this cluster, see
http://www.genoscope.cns.fr/
csl-bin/cluster.cgi?seq=CS0DJ003DE05NP1&cluster=261.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :

CD642093 AGENCOURT
AY420372 Homo sapi
BG572311 602594534
BG544257 602586034
AK036407 Mus muscu
AV714060 AV714060
AV716055 AV716055
AV714044 AV714044
CF181629 818478 MA
CD466872 Leukon2.8
AQ317367 RPI11-10
AV715708 AV715708
CB553797 MNSP0073
CD468328 Leukos3.2
BG253969 602366484
CD468976 Leukos3.8
AV712845 AV712845
AY420373 Pan trogl
AY420374 Mus muscu
AQ053459 RPI11-50
BU698389 LI21n1395
CD465070 Leukon1.1
AA195206 z34h12.f
AQ887601 HS 5557.A
W04905 za3510.r1
BM145481 TCAAP1D53
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N98410 za69c05.r1
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BU361362 603788927
BM146419 TCAAP1E47
CD465007 Leukon1.1
NS9342 yz86e03.s1
CD468899 Leukos3.8
BG625427 pgnlc.pko

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DJ003DE05NFI.

FEATURES

Location/Qualifiers
1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ003YJ10"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 45.0%; Score 998.2; DB 9; Length 1201;
Best Local Similarity 95.1%; Pred. No. 1.2e-135;
Matches 1010; Conservative 22; Mismatches 29; Indels 1; Gaps 1;

QY	1045	TTCTGTAAACCTCTTATTTGATGTCATTCATTCATTAATACGAAAAAACTTATTTCT	1104
DB	1063	TWTCTGTAAACCTCTTATTTGATGTCATTCATTCATTAATACGAAAAAACTTATTTCT	1005
QY	1105	TAATCAAAAGGCGAGTACAAAAAGTAATATGTTTATAGATGTTAGTAAAGTAA	1164
DB	1004	TATCAAAAGGCGAGTACAAAAAGTAATATGTTTATAGATGTTAGTAAAGTAA	945
QY	1165	AGTTAAGCTTTTGCAGAGTTGTCAAAAGTTCACAAAGTCTAGTTCGGATTTTACC	1224
DB	944	AGTTAAGCTTTTGCAGAGTTGTCAAAAGTTCACAAAGTCTAGTTCGGATTTTACC	885
QY	1225	AAAGCGATATATGTTTATATAACATATATATCTAGATATCAAAATGTTTCAGAT	1284
DB	884	AAAGCGATATATGTTTATATAACATATATATCTAGATATCAAAATGTTTCAGAT	825
QY	1285	AGCATTTTTCATAAGTCTCTCTTTTGGTAAATAGTGTAGAGATGATCTGGTTC	1344
DB	824	AGCATTTTTCATAAGTCTCTCTTTTGGTAAATAGTGTAGAGATGATCTGGTTC	765
QY	1345	TTACAATGGAGATGAAGAACATTTATTTATGGTGTACTACTAACCTGTCCAGATA	1404
DB	764	TTACAATGGAGATGAAGAACATTTATTTATGGTGTACTACTAACCTGTCCAGATA	705
QY	1405	GTAATATCACTCTAGTTATAGCCAGCAACAGGAACCTTTTGTGAAGACATTCATCTC	1464
DB	704	GTAATATCACTCTAGTTATAGCCAGCAACAGGAACCTTTTGTGAAGACATTCATCTC	645
QY	1465	TACAGAACTTCAGATTAATAATCTAGATTAATGACTGAGAATAAGATCCACATTTGA	1524
DB	644	TACAGAACTTCAGATTAATAATCTAGATTAATGACTGAGAATAAGATCCACATTTGA	585
QY	1525	ACTCATCTAGTGAACATGACGTACCCAGTATACAAAGTACTCTCTGTGGTGCACAG	1584
DB	584	ACTCATCTAGTGAACATGACGTACCCAGTATACAAAGTACTCTCTGTGGTGCACAG	525
QY	1585	AAACATGACCGATTTTGCATATCTCCAGTGGGAACCTAAGTAGACTACCTTATCACCG	1644
DB	524	AAACATGACCGATTTTGCATATCTCCAGTGGGAACCTAAGTAGACTACCTTATCACCG	465
QY	1645	GCTAAGAAACCTGCTACTAACTATTAGCCATCAATGCTGTGTAATAAACCAGAGAA	1704
DB	464	GCTAAGAAACCTGCTACTAACTATTAGCCATCAATGCTGTGTAATAAACCAGAGAA	405
QY	1705	GGTTTTTCCAGGACGCTCTCATGTTTGGCCCTTTTGAATTTGGGTAGAAATCAGAAATGA	1764
DB	404	GGTTTTTCCAGGACGCTCTCATGTTTGGCCCTTTTGAATTTGGGTAGAAATCAGAAATGA	345
QY	1765	GATGAGGGAAGAAGCAAGAGTCTTAAGCCCTTAGCGATTTGGCATCTGCCACATTTGGT	1824
DB	344	GATGAGGGAAGAAGCAAGAGTCTTAAGCCCTTAGCGATTTGGCATCTGCCACATTTGGT	285

QY	1825	TCATATTCAGAAAGTCTTATCTCATTGATTATATATCTTCTTAAAGCAAAATCTCCTTAAGTA	1884
DB	284	TCATATTCAGAAAGTCTTATCTCATTGATTATATATCTTCTTAAAGCAAAATCTCCTTAAGTA	225
QY	1885	ATTATTATTCAAAATAAGATTATATCTACATCATCATCTATATCTCTGTTTAAAGAGATATT	1944
DB	224	ATTATTATTCAAAATAAGATTATATCTACATCATCATCTATATCTCTGTTTAAAGAGATATT	165
QY	1945	TAATTTTAAATGCTGTTTACATGCTGTAATATTTTAAATATTTTAAATATGATCCATCATTA	2004
DB	164	TAATTTTAAATGCTGTTTACATGCTGTAATATTTTAAATATTTTAAATATGATCCATCATTA	105
QY	2005	GGCTTTGGAAATTTAAATGTTAGTTGAAATGTAATATGTAATATGTAATATGTAATATGTAAT	2064
DB	104	GGCTTTGGAAATTTAAATGTTAGTTGAAATGTAATATGTAATATGTAATATGTAATATGTAAT	45
QY	2065	TAATAAATATTTTAACTTCATTCATACATACAGTTAAGTTTATCT	2106
DB	44	TAATAAATATTTTAACTTCATTCATACATACAGTTAAGTTTATCT	3

RESULT 2
AL557903 1201 bp mRNA linear EST 31-MAY-2003
AL557903 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS0DJ003YJ10 5-PRIME, mRNA sequence.

ACCESSION AL557903
VERSION AL557903.2
KEYWORDS EST, GI:1279703
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
1 (bases 1 to 1201)
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12901962.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 261.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DJ003DE05QF&cluster=261.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DJ003DE05QF1.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ003YJ10"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 41.4%; Score 918.2; DB 9; Length 1201;
Best Local Similarity 97.0%; Pred. No. 4.9e-124;
Matches 938; Conservative 7; Mismatches 20; Indels 2; Gaps 1;
QY 61 ATAACTTTTATCTACTATGATATGATGGAATAGTATTATAAATGAACCTAGGAAG 120

Db 110 ATAACCTTTTATTCTACTATGATATGATGTAAGAAAGTATTAATAAATGAACATAGGGAAG 169
QY 121 GATGTAATAAATAGACATCTCTTCAATTTAGAGAGAAAGATGGAACAAACATTTGCTTTTC 180
Db 170 GATGTAATAAATAGACATCTCTTCAATTTAGAGAGAAAGATGGAACAAACATTTGCTTTTC 229
QY 181 TTTTCTCAATAAATATGTCGAATCAAAAGAAACCTTTTTCCTCAAGTTTAAATACATGGT 240
Db 230 TTTTCTCAATAAATATGTCGAATCAAAAGAAACCTTTTTCCTCAAGTTTAAATACATGGT 289
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QY 301 CTAAGCTCTCTGTCAGAAACCTCAGTTTCATGAGACACCCGCTCAGTAGATCTGGG 360
Db 350 CTAAGCTCTCTGTCAGAAACCTCAGTTTCATGAGACACCCGCTCAGTAGATCTGGG 409
QY 361 CACTTGGCCAAAGAAACAAAGAGTCTCCCTGAAGAGGAGTGAATGGGGTGAATCAATT 420
Db 410 CACTTGGCCAAAGAAACAAAGAGTCTCCCTGAAGAGGAGTGAATGGGGTGAATCAATT 469
QY 421 GACAACTGCTTTCCCATAGAGATGAGTACAGGCTTTTACAGATTTCTTTAAACTGAA 480
Db 470 GACAACTGCTTTCCCATAGAGATGAGTACAGGCTTTTACAGATTTCTTTAAACTGAA 529
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Db 530 TTCAGTGAAGAAATATTAATTTTGGATAGCTGTGAAGATTTCAAGAAAGCAAGGA 589
QY 541 CCTCAACAAATCAGCTTAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCC 600
Db 590 CTTCAACAAATCAGCTTAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCC 649
QY 601 CCAAAAGAGGTTTAACTGATTTTACACAAAGAAAGTCATTACAAACAGCATCACTCAA 660
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Db 890 CAATCAGATGTTGCCATTTGTTATTAAGAAATTTGATTTTGTCTCATTTTATGACAAAC 949
QY 901 TTATACATCTGCTTCTAATCATGCTGTTTATGTTTAAAGATTTGGTCCCATCTTTAAA 960
Db 950 TTATACATCTGCTTCTAATCATGCTGTTTATGTTTAAAGATTTGGTCCCATCTTTAAA 1007
QY 961 CTGAATATGTCATGTAATTTATTTTAAATGTAAACAAACAAACCTTTCTGCTTAACAAA 1020
Db 1008 CTGAATATGTCATGTAATTTATTTTAAATGTAAACAAACAAACCTTTCTGCTTAACAAA 1067
QY 1021 ATACATA 1027
Db 1068 ATAMGA 1074

RESULT 3
BX349093
LOCUS BX349093 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION BX349093 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cDNA clone CS00J003VJ10 5-PRIME, mRNA sequence.
ACCESSION BX349093

VERSION BX349093.1 GI:30375347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 261.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAG041ZE09_CS03909_1&cluster=261.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0BAG041ZE09_CS03909_1.
FEATURES
Location/Qualifiers
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/clone="CS0DJ003VJ10"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the PCWSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 39.3%; Score 872.2; DB 13; Length 923;
Best Local Similarity 97.8%; Pred. No. 2.6e-117;
Matches 902; Conservative 0; Mismatches 18; Indels 2; Gaps 2;
QY 865 TAAAGAAATGATTTTGTCTCATTTTATGACAACTTATACATCTGCTTCAACATATC 924
Db 2 TTAAGAAATGATTTTGTCTCATTTTATGACAACTTATACATCTGCTTCAACATATC 61
QY 925 GCATGTTTATGTTAAGATTGGTCCCATCTTTTAAACTGAAATATGCTGCAAAATTAT 984
Db 62 GCATGTTTATGTTAAGATTGGTCCCATCTTTTAAACTGAAAT-TGTCATGTGAATTTAT 120
QY 985 TTTAAATATGTAATAAACAACAACTTTCTGCTTAACAAATACATACATATCTGCCAGTATA 1044
Db 121 TTTAAATATGTAATAAACAACAACTTTCTGCTTAACAAATACATACATATCTGCCAGTATA 180
QY 1045 TTTCTGTAAACCTCTTATTTGATGTCATTTCCATTTTATATATCAAGAAAAAATTTTCT 1104
Db 181 TTTCTGTAAACCTCTTATTTGATGTCATTTCCATTTATATATCAAGAAAAAATTTTCT 240
QY 1105 TAAATCAAGGCGAGTCAAAAAAGTAATAATGTTTTATAAGATTGTAGAGTTAAGTAA 1164
Db 241 TAAATCAAGGCGAGTCAAAAAAGTAATAATGTTTTATAAGATTGTAGAGTTAAGTAA 300
QY 1165 AGTTAAGCTTTTCAAGATTGTCAAAAGTTCAACAAAGTCTAGTTGGATTTTACC 1224
Db 301 AGTTAAGCTTTTCAAGATTGTCAAAAGTTCAACAAAGTCTAGTTGGATTTTACC 360
QY 1225 AAAGCAGCATATATGTTTATATAAACAATAATACTCAGATATCCAAATGTTCCAGAT 1284
Db 361 AAAGCAGCATATATGTTTATATAAACAATAATACTCAGATATCCAAATGTTCCAGAT 420
QY 1285 AGCATTTTTCATTAATGAATGTTCTCTTTTGGTAAATAGTGTAGAAAGTATCTGGTTC 1344
Db 421 AGCATTTTTCATTAATGAATGTTCTCTTTTGGTAAATAGTGTAGAAAGTATCTGGTTC 480

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Sma I sites of the pCMVSPORT 6 vector. Library was normalized.

```

ORIGIN
Query Match      31.0%; Score 688.2; DB 13; Length 921;
Best Local Similarity 94.0%; Pred. No. 1.2e-90;
Matches 758; Conservative 0; Mismatches 44; Indels 4; Gaps 4;

QY 1345 TTACAATGGGAGATGAAGAACATTTTATTATTGGGTACTACTAACCTGTGCCAAGAATA 1404
Db 481 TTACAATGGGAGATGAAGAACATTTTATTATTGGGTACTACTAACCTGTGCCAAGAATA 540

QY 1405 GTAATATACCTCTAGTTAATAGCCAGCAACAGGAACCTTTGTGAAGACATTCATCTC 1464
Db 541 GTAATATACCTCTAGTTAATAGCCAGCAACAGGAACCTTTGTGAAGACATTCATCTC 600

QY 1465 TACAGAACTTCAGATTAAATATAAATCTAGATTAAATAGCTAGAGATAAGATCCACATTGA 1524
Db 601 TACAGAACTTCAGATTAAATATAAATCTAGATTAAATAGCTAGAGATAAGATCCACATTGA 660

QY 1525 ACTCATTTCTAAGTGAACATGGACGTACCCAGTTATACAAAGTACTTCTGTGTGTCACAG 1584
Db 661 ACTCATTTCTAAGTGAACATGGACGTACCCAGTTATACAAAGTACTTCTGTGTGTCACAG 720

QY 1585 AAACATGACCAATTTTGCATATCTCCAGTAGGAACTAAGTACCTACCTTATCACCG 1644
Db 721 AAACATGACCAATTTTGCATATCTCCAGTAGGAACTAAGTACCTTATCACCG 780

QY 1645 GCTAAGAAACCTTGCTACTATAACTATTAGGCCATCAATGGCTTGAATATAAACCAGAGAA 1704
Db 781 NCTAAGAAACCTTGCTACTATAACTATTAGGCCATCAATGGCTTGAATATAAACCAGAGAA 840

QY 1705 GGTGTTTCCAGGAGCTCTCATG-TTGGCCCTTTAGAAATGGGGTAGAAATCAGAAATG 1763
Db 841 GNTTTTCCAGGAGCTCTCATG-TTGGCCCTTTAGAAATGGNNGTAGAAATCAGAAATG 900

QY 1764 AGATGAGGGAAGAGAGCAAGGA 1785
Db 901 AGATGAGGGAAGAGCAAGGA 922

RESULT 4
BX350311/c
LOCUS
DEFINITION
Homo sapiens cDNA clone CS0DJ03YJ10 3-PRIME, mRNA sequence.
ACCESSION
BX350311
VERSION
BX350311.1 GI:30373474
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Web : www.genoscope.cns.fr
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 261.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BA10322C02_CS02987_1&cluster=261.f.
Contact : Feng Liang Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BA10322C02_CS02987_1.
Location/Qualifiers
1. .921
/organism="Homo sapiens"
/mol_type="mRNA"
/ab_xref="taxon:9606"
/clone="CS0DJ03YJ10"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)

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FEATURES
source

RESULT 5
CD642093
LOCUS
DEFINITION
AGENCOURT_14536786 NIH_MCC_191 Homo sapiens cDNA clone
IMAGE:30418254 5', mRNA sequence.
ACCESSION
CD642093
VERSION
CD642093.1 GI:31811624

CD642093 703 bp mRNA linear EST 17-JUN-2003
AGENCOURT_14536786 NIH_MCC_191 Homo sapiens cDNA clone
IMAGE:30418254 5', mRNA sequence.
CD642093
CD642093.1 GI:31811624

Db	303	AAATGTTTCAGATAGCAATTTTTCATAATGAATGTTCTCTTTTTCGTAATAGTGTAGAA	362	
Qy	1333	GTGATCTGGTCTTACAAATGGGAGATGAAGAACATTTATTATTGGTGTACTACTAACCCCT	1392	
Db	363	GTGATCTGGTCTTACAAATGGGAGATGAAGAACATTTATTATTGGTGTACTACTAACCCCT	422	
Qy	1393	GTCCCAAGAATAAGTAATATACCTCTCTAGTTATAAGCCAGCAACAGGAACATTTTGTGAAGA	1452	
Db	423	GTCCCAAGAATAAGTAATATACCTCTCTAGTTATAAGCCAGCAACAGGAACATTTTGTGAAGA	482	
Qy	1453	CACATTTCATCTCTACAGAACTTCAGATTAATAATATAATCTAGATTAATGACTGAGAATAAG	1512	
Db	483	CACATTTCATCTCTACAGAACTTCAGATTAATAATATAATCTAGATTAATGACTGAGAATAAG	542	
Qy	1513	ATCCACATTGGAACCTCATCTCTAAGTAGACATGACGAGTACCCAGTTATACAAAGTACTTC	1572	
Db	543	ATCCACATTGGAACCTCATCTCTAAGTAGACATGACGAGTACCCAGTTATACAAAGTACTTC	602	
Qy	1573	TGTTGGTCCAGCAAAACATGACCATGTTTGCATATCTCCAGTAGGAGAACTTAAGTAGACT	1632	
Db	603	TGTTGGTCCAGCAAAACATGACCATGTTTGCATATCTCCAGTAGGAGAACTTAAGTAGACT	662	
Qy	1633	ACCTTATCACCGGCTAAGAAACTTGTCTACTAAACTATTA	1672	
Db	663	ACCTTATCACCGGCTAAGAAACTTGTCTACTAAACTATTA	702	
RESULT 6	AY420372	708 bp	DNA linear	GSS 12-DEC-2003
LOCUS	Homo sapiens HCM7202 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.			
DEFINITION	AY420372			
ACCESSION	AY420372.1	GI:39776329		
VERSION	GSS.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 708)			
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science 302 (5652), 1960-1963 (2003)			
PUBMED	14671302			
REFERENCE	2 (bases 1 to 708)			
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
COMMENT	This sequence is made by sequencing genomic exons and ordering them based on alignment.			
FEATURES	Location/Qualifiers			
source	1..708			
gene	/organism="Homo sapiens"			
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ORIGIN	/locus_tag="HCM7202"			
Query Match	29.5%;	Score 655;	DB 29;	Length 708;
Best Local Similarity	92.5%;	Pred. No. 9.3e-86;		
Matches	655;	Conservative 0;	Mismatches 53;	Indels 0;
Gaps	0;			
Qy	160	ATGGAAACCAACATCTCTTTTCTCTCAATAATATGTTGATCAAGAAAAA	219	

Db 1 ATGGAAACAACATTCGCTTTCTTTCTCAATATATGTGTGAATCAAAAGAAACACT 60
 Qy 220 TTTTTCAGTTTAAATACATGGTTTCAGAAAGAGAAACAGCAAGAGAGCCAAATCAGA 279
 Db 61 TTTTTCAGTTTAAATACATGGTTTCAGAAAGAGAAACAGCAAGAGAGCCAAATCAGA 120
 Qy 280 GCTAAGGAAAAAGAAATAGACTTCTTTCTGTCAGAAACCTGAGTTTCATGAAGAC 339
 Db 121 GCTAAGGAAAAAGAAATAGACTTCTTTCTGTCAGAAACCTGAGTTTCATGAAGAC 180
 Qy 340 ACCCGTCCAGTAGATTCGGGCACTTGGCCAAAGAAACAGAGTCTCCCTCAGAGAGCA 399
 Db 181 ACCCGTCCAGTAGATTCGGGCACTTGGCCAAAGAAACAGAGTCTCCCTCAGAGAGCA 240
 Qy 400 GTGAATGGGGTGAATCATTTTACAAACCTGCTTCCCATAGAGATGGACTAGAGCTTTT 459
 Db 241 GTGAATGGGGTGAATCATTTTACAAACCTGCTTCCCATAGAGATGGACTAGAGCTTTT 300
 Qy 460 ACCAGATTCTTTAAACTGAATTCAGTGAAGAAATATGTAATTTTGGATGACCTGTGAA 519
 Db 301 ACCAGATTCTTTAAACTGAATTCAGTGAAGAAATATGTAATTTTGGATGACCTGTGAA 360
 Qy 520 GAATTCAGAAAGCAAGGACCTCAACAAATTCACCTTAAGCAAGCAATATATGAG 579
 Db 361 GAATTCAGAAAGCAAGGACCTCAACAAATTCACCTTAAGCAAGCAATATATGAG 420
 Qy 580 AAATTTATACAGATGATGCCCAAGAGGTTAACTTGTGATTTTACACAAAGAAAGTC 639
 Db 421 NNN 480
 Qy 640 ATTACAAACAGATCACTCAACTACCTCCACAGTTTTCATGCTGCAAGAGAGAGTG 699
 Db 481 ATTACAAACAGATCACTCAACTACCTCCACAGTTTTCATGCTGCAAGAGAGAGTG 540
 Qy 700 TATCAGCTCATGGAAACAGACAGTTATACACGTTTCTGAAATCTGACATCTATTAGAC 759
 Db 541 TATCAGCTCATGGAAACAGACAGTTATACACGTTTCTGAAATCTGACATCTATTAGAC 600
 Qy 760 TTGATGGAAGGAGACCTCAGAGCAACAAATCTTAGAGAGCATCAGCTCATTTACC 819
 Db 601 TTGATGGAAGGAGACCTCAGAGCAACAAATCTTAGAGAGCATCAGCTCATTTACC 660
 Qy 820 TSCAATGAATTCGAAGATGCAATCAGATGTTGCCATTTGGTTATAA 867
 Db 661 TSCAATGAATTCGAAGATGCAATCAGATGTTGCCATTTGGTTATAA 708

RESULT 7
 BG572311
 LOCUS 655 bp mRNA linear EST 10-APR-2001
 DEFINITION 602594534P1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4721624 5',
 mRNA sequence.
 ACCESSION BG572311
 VERSION BG572311.1 GI:13579964
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue procurement: CLONTECH Laboratories, Inc.
 cDNA library preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1578 row: d column: 09

FEATURES
 source 1..655
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4721624"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_79"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
 Site1: SfiI (ggcccttggcc); Site2: SfiI
 (ggccattatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.3
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 29.0%; Score 643; DB 12; Length 655;
 Best Local Similarity 99.8%; Pred. No. 5.4e-84;
 Matches 65; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1242 GTTATATAACATAATACTCAGATATCCAAATGTTCCAGATAGCATTTTTCATAATGA 1301
 Db 1 GTTATATAACATAATACTCAGATATCCAAATGTTCCAGATAGCATTTTTCATAATGA 60
 Qy 1302 ATGTTCTCTTTTGGTAAAGTAGTGTAGAGTGTCTGGTTCTTACATGGAGATGAA 1361
 Db 61 ATGTTCTCTTTTGGTAAAGTAGTGTAGAGTGTCTGGTTCTTACATGGAGATGAA 120
 Qy 1362 GAACATTTTATTTGGTTTACTACTAACCTGTGCCAAGATAGTAATATCACTCTAGT 1421
 Db 121 GAACATTTTATTTGGTTTACTACTAACCTGTGCCAAGATAGTAATATCACTCTAGT 180
 Qy 1422 TATAAGCCAGCAACAGAACTTTTGAAGACACATTCATCTCTACAGAACTTCAGATTA 1481
 Db 181 TATAAGCCAGCAACAGAACTTTTGAAGACACATTCATCTCTACAGAACTTCAGATTA 240
 Qy 1482 AATATAATCTAGATTAATGACTGAGAAATAGATCCACATTTGAACTCATCTCTAAGTGAA 1541
 Db 241 AATATAATCTAGATTAATGACTGAGAAATAGATCCACATTTGAACTCATCTCTAAGTGAA 300
 Qy 1542 CATGGAAGTACCCAGTTATACAAAGTACTTGTGGTCAAGAAACATGACAGATTTT 1601
 Db 301 CATGGAAGTACCCAGTTATACAAAGTACTTGTGGTCAAGAAACATGACAGATTTT 360
 Qy 1602 GCATATCTCCAGTACGGAACTAAAGTAGACTACCTTATCACCGGCTAAGAAACCTTGCTA 1661
 Db 361 GCATATCTCCAGTACGGAACTAAAGTAGACTACCTTATCACCGGCTAAGAAACCTTGCTA 420
 Qy 1662 CTAACACTATTAGCCCATCAATGGCTTTGAATAAACCAGAGAGGTTTTCOCAGAGCT 1721
 Db 421 CTAACACTATTAGCCCATCAATGGCTTTGAATAAACCAGAGAGGTTTTCOCAGAGCT 480
 Qy 1722 CTCATGTTGGCCCTTAGAATGGGTAGAAATCAGAAATCAGATGAGGGGAAGAA-OC 1780
 Db 481 CTCATGTTGGCCCTTAGAATGGGTAGAAATCAGAAATCAGATGAGGGGAAGAA-OC 540
 Qy 1781 AAGGAGTCTAAGGCCCTTAGCGATTTGGGCATCTGCCACATTTGGTTCATATTCAGAAAGTG 1840
 Db 541 AAGGAGTCTAAGGCCCTTAGCGATTTGGGCATCTGCCACATTTGGTTCATATTCAGAAAGTG 600
 Qy 1841 TTATCTCATGTATTATATCTTGTGAAGCAATCTCCTTAAGTATATTTATTTCA 1895
 Db 601 TTATCTCATGTATTATATCTTGTGAAGCAATCTCCTTAAGTATATTTATTTCA 655

RESULT 8
 BG564257

JOURNAL REFERENCE AUTHORS	Nature 409, 695-690 (2001)	Db	89	TTTATTGAGGATGTTTCTTATCAATAGCATTCATCTGTGGAGAGAGAGGAGTAAGG	148
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Qy	129	AAATTGAGCATCTCTTCAT--TTTAGAGAGAGATGGAACAACATGCTTTTCTTTCT	186
JOURNAL REFERENCE AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Db	149	AAATCTGACATCTGTTGGTCACTGGGACAGATATGATGCTGCTTTCTTCTCT	208
TITLE	Nature 420, 563-573 (2002)	Qy	187	CAATAAATATGTTGAATCAAAAGAAAAAATCTTTTCAAGTTAATACATGTTTCA	246
JOURNAL REFERENCE AUTHORS	6 (bases 1 to 1860)	Db	209	CAATTAATATGTTGAATCAAAAGAAAAAATCTTTTCAACTAATGATGGTTCAGG	268
TITLE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saibata, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	Qy	307	CTTCTTGTGCGAAGAACTGAGTTTCAATGAAGACACCGCTCCAGTAGATCTGGGAC	366
JOURNAL REFERENCE AUTHORS	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	Db	329	CTTCTCTCAGAGGCTGACITTCATGGAGAGACTCAAGCCAGTAGATCTGCCCTCT	388
TITLE	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	Qy	367	GCCAAAGAAACAGAGTCTCCCTGAAAGAGGAGTGAATGGGTGAATCATTTGACAA	426
JOURNAL REFERENCE AUTHORS	Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers	Db	389	GCCAAAGAAACAGAGTCTCTCTGAAGAGCAGTGAATGGCTGATCATTTGACAA	448
COMMENT	1. .1860 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM.DB:9830006J10" /db_xref="MGI:2400834" /db_xref="taxon:10090" /clone="9830006J10" /sex="male" /tissue_type="bone" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 182..889	Qy	427	CTCCTTCCCATAGAGATGAGCTAGAGGCTTTTACAGATTTCTTAAACTGAATTCAG	486
FEATURES	source	Db	449	TTGCTCTCTCATAGAGATGGAGTGGATGCTTTTACAGATTTCTTAAACTGAATTCAG	508
		Qy	487	GAAGAAATATTGAATTTTGGATAGCTCTGGAAGATTTCAAGAAAGCAAGGACCTCA	546
		Db	509	GAGGAGAACTGAAATTTGGTGGCTGTGAAGACTTCAAGAAATGCAAGAACTCA	568
		Qy	547	CAAAATCAGCTTAAAGCAAAAGCAATATATAGAAATTTATACAGACTGATCCCCAAA	606
		Db	569	CAAAATCATCTAAAGCAAAAGCAATCTATGAAATTCATTTCAGAAATGATCCCCAAA	628
		Qy	607	GAGGTTAACTGATTTTCCACAAAGAGTCATTACAAACAGATCATCAACTACC	666
		Db	629	GAGGTTAACTGATTTTCCACAAAGAGTCATTACAAACAGATCATCAACTACC	688
		Qy	667	CTCCAGATTTTGAAGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAGAGTTAT	726
		Db	689	CTCCAGATTTTGAAGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAGAGTTAT	748
		Qy	727	ACAGCTTTTCTGAATCTGACATCTATTTAGACTTGTAGAGAGGAGACCTCAGAGCA	786
		Db	749	AAACGCTTTTGAATCTGACACTTACTTACATTTGATAGAGGAGAGCTCAGAGCA	808
		Qy	787	ACAAATCTTAGGAGAGATCAGCTCATTTTACCTGCAATGAATTTCAAGATGACAATCA	846
		Db	809	ACAACTTTAGGAGAGATCAGCTCATTTTACCTGCAATGAATTTCAAGATGACAATCA	868
		Qy	847	GATGTTGCCATTTGGTTTAAAGAAAATTTGATTTTGTCTCATTTTATGCAAACTTATAC	906
		Db	869	GATGTTGCCATTTGGTTTAAAGAAAATTTGATTTTGTCTCATTTTATGCAAACTTATAC	928
		Qy	907	ATC-----TGCTTTAAACATATCGCATGTTTATGTTAAGA	941
		Db	929	AUTAAATATATATACTAATACTAAATGTTTCTTAAATATAGCTTGTGATAGAAGA	988
		Qy	942	TTTGGTCCATCTTTAAACTGAAATATGTCATGTAAGAAATTTTAAATAAGTAAAAAC	1001
		Db	989	GATGATTTTCAATTT-----TAAATAACACCATGCAATATACATATAATGTAAGA	1042
		Qy	1002	AAACCTTTCTGCTTAAACAAATACATACAGTATCTCCAGTATATTTCTGTAACCTCTTA	1061
		Db	1043	TTTATATATATACATAAATAATATTCATCTATCTTCCGAAATATTTTATGAAATCTATC	1102
		Qy	1062	TTTGATGTCATCCATTTTATAATCAGAAAAAAACTTATTTCTTAATCAAAAGGAGTAC	1121
		Db	1103	TGATATTTCTTAAATAAATTTCTTATTTCTACATAACAGTCAAGTAAGAAGAGCTT	1162
		Qy	1122	AAAAAGTAAATGTTTATAGATTTAGAGTTAGTAAAGTAAAGTCTTTTGCATA	1181
		Db	1163	TGTAATTTGTAAGTAAATGAAACCTTTGTAGTAATGTACATCTAGTTTGGATTATA	1222
ORIGIN	Query Match 26.9%; Score 596; DB 11; Length 1860; Best Local Similarity 72.1%; Pred. No. 1.8e-77; Matches 833; Conservative 290; Mismatches 290; Indels 33; Gaps 3;	Qy	69	TTATTTCTACTATGTTATGTTAGTAATGATGTTAATTAATGAACCTAGGAGGATGTAAT	128

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QY 1182 GTGTCAAAAGTCTAA 1197
Db 1223 TTTCTAAGCAAGCAA 1238

RESULT 10
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LOCUS AV714060 DCB Homo sapiens cDNA clone DCBBIF02 5', mRNA sequence.
DEFINITION AV714060
ACCESSION AV714060
VERSION AV714060.1 GI:10795577
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 705)
XU.X., GU.J., LIU.F., QU.J., ZHAO.M., LI.Y., HUANG.Q., ZHOU.J.,
SONG.H., GU.Y., YANG.Y., GAO.G., XIAO.H., LI.N., QIAN.B., GAO.X.,
CHENG.Z., XU.S., GU.W., TU.Y., JIA.J., FU.G., REN.S., ZHONG.M.,
LU.G., CHENG.Z. and HAN.Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
Location/Qualifiers
1..705
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBBIF02"
/dev_stage="dendritic cells"
/lab_host="BM25.8"
/clone_lib="DCB"
/note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"
ORIGIN
Query Match 25.6%; Score 568; DB 9; Length 705;
Best Local Similarity 96.5%; Pred. No. 3.8e-73;
Matches 580; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 61 ATAACTTTTATCTACTATGTATGTATGTAATGTAATTAATAAATGAACTAGGGAAG 120
Db 71 ATAACTTTTATCTACTATGTATGTATGTAATGTAATTAATAAATGAACTAGGGAAG 130

QY 121 GATGTAATAAATAGACATCTCTTCATTTTAGAGAGAGATGGAACAAACATTCCTTTTC 180
Db 131 GATGTAATAAATAGACATCTCTTCATTTTAGAGAGAGATGGAACAAACATTCCTTTTC 190

QY 181 TTTTCTCAATAAATATGTGTGTAATCAAAAGAAAACCTTTTTCAGTTAATACATGGT 240
Db 191 TTTTCTCAATAAATATGTGTGTAATCAAAAGAAAACCTTTTTCAGTTAATACATGGT 250

QY 241 TCAGGAAAGAGAAACCAAGCAAGAACCCAAAATCAGAGCTAAGGAAAGAAAGAAATAGA 300
Db 251 TCAGGAAAGAGAAACCAAGCAAGAACCCAAAATCAGAGCTAAGGAAAGAAAGAAATAGA 310

QY 301 CTAAGTCTTCTTGTCAGAAACCTGAGTTTCATGAGACACCCGCTCCAGTAGATCTGGG 360
Db 311 CTAAGTCTTCTTGTCAGAAACCTGAGTTTCATGAGACACCCGCTCCAGTAGATCTGGG 370

QY 361 CACTTGGCAAGAAACCAAGAGTCTCCCTCAAGAGGAGTGAATGGGGTGAATCATTT 420
Db 371 CACTTGGCAAGAAACCAAGAGTCTCCCTCAAGAGGAGTGAATGGGGTGAATCATTT 430

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QY 421 GACAAACTGCTTTCCCATAGAGATGAGGCTTTTACCAGATTTCTTAAACTGAA 480
Db 431 GACAAACTGCTTTCCCATAGAGATGAGGCTTTTACCAGATTTCTTAAACTGAA 490

QY 481 TTCAGTGAAGAAATATTTGAATTTTGGATAGCCTGTGAAGATTTCAAGAAAAGCAAGGGA 540
Db 491 TTCAGTGAAGAAATATTTGAATTTTGGATAGCCTGTGAAGATTTCAAGAAAAGCAAGGGA 550

QY 541 CCTCAACAATTCACCTTAAAGCAAGCAATATATGAGAAATTTTATACAGACTGATGCC 600
Db 551 CCTCAACAATTCACCTTAAAGCAAGCAATATATGAGAAATTTTATACAGACTGATGCC 610

QY 601 CCAAAAAGAGTTAACCTTGAATTTTACACAAAGAAGTCAATACAAACAGCATCACTCAA 660
Db 611 CCAAAAAGAGTTAACCTTGAATTTTACACAAAGAAGTCAATACAAACAGCATCACTCAA 670

QY 661 C 661
Db 671 C 671

RESULT 11
AV716055 639 bp mRNA linear EST 11-OCT-2000
LOCUS AV716055 DCB Homo sapiens cDNA clone DCBBOD01 5', mRNA sequence.
DEFINITION AV716055
ACCESSION AV716055
VERSION AV716055.1 GI:10797572
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 639)
XU.X., GU.J., LIU.F., QU.J., ZHAO.M., LI.Y., HUANG.Q., ZHOU.J.,
SONG.H., GU.Y., YANG.Y., GAO.G., XIAO.H., LI.N., QIAN.B., GAO.X.,
CHENG.Z., XU.S., GU.W., TU.Y., JIA.J., FU.G., REN.S., ZHONG.M.,
LU.G., CHENG.Z. and HAN.Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
Location/Qualifiers
1..639
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBBOD01"
/dev_stage="dendritic cells"
/lab_host="BM25.8"
/clone_lib="DCB"
/note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"
ORIGIN
Query Match 25.5%; Score 565.4; DB 9; Length 639;
Best Local Similarity 99.5%; Pred. No. 9.6e-73;
Matches 566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 61 ATAACTTTTATCTACTATGTATGTATGTAATGTAATTAATAAATGAACTAGGGAAG 120
Db 71 ATAACTTTTATCTACTATGTATGTATGTAATGTAATTAATAAATGAACTAGGGAAG 130

QY 121 GATGTAATAAATAGACATCTCTTCATTTTAGAGAGAGATGGAACAAACATTCCTTTTC 180
Db 131 GATGTAATAAATAGACATCTCTTCATTTTAGAGAGAGATGGAACAAACATTCCTTTTC 190

QY 181 TTTTCTCAATAAATATGTGTGTAATCAAAAGAAAACCTTTTTCAGTTAATACATGGT 240

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|||||
Db 191 TTTTCTCAATTAATATGTGTGAATCAAGAGAAAACCTTTTCAAGTTAATACATGGT 250
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Qy 241 TCAGGAAAGAGAAACCAAGCAAGCAAGCCAAATCAGAGCTAAGGAAAAGAAATAGA 300
|||||
Db 251 TCAGGAAAGAGAAACCAAGCAAGCAAGCCAAATCAGAGCTAAGGAAAAGAAATAGA 310
|||||
Qy 301 CTAAGTCTTCTGTGCAGAAACCTGAGTTTCATGAAGACACCCGCTCCAGTAGATCTGGG 360
|||||
Db 311 CTAAGTCTTCTGTGCAGAAACCTGAGTTTCATGAAGACACCCGCTCCAGTAGATCTGGG 370
|||||
Qy 361 CACTTGGCCAAAGAAACCAAGAGTCTCCCTCGAAGAGCAGTGAAATGGGGTGAATCATTT 420
|||||
Db 371 CACTTGGCCAAAGAAACCAAGAGTCTCCCTCGAAGAGCAGTGAAATGGGGTGAATCATTT 430
|||||
Qy 421 GACAACTGCTTTCCCATAGAGTGGCTAGAGGCTTTTACCAGATTTCTTAAACTGAA 480
|||||
Db 431 GACAACTGCTTTCCCATAGAGTGGCTAGAGGCTTTTACCAGATTTCTTAAACTGAA 490
|||||
Qy 481 TTCAGTGAAGAAATATTCAAATTTTGGATAGCTGTGAAGATTTCAAGAAAAGCAAGGGA 540
|||||
Db 491 TTCAGTGAAGAAATATTCAAATTTTGGATAGCTGTGAAGATTTCAAGAAAAGCAAGGGA 550
|||||
Qy 541 CTTCAACAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGACTGATGCC 600
|||||
Db 551 CTTCAACAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGACTGATGCC 610
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Qy 601 CCAAAAGAGGTTAACTTGAATTTTCACAC 629
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Db 611 CCAAAAGAGGTTAACTTGAATTTTCACAC 639

```

RESULT 12

AV714044 626 bp mRNA linear EST 11-OCT-2000
 LOCUS AV714044 DCB Homo sapiens cDNA clone DCBCHF06 5', mRNA sequence.

ACCESSION AV714044
 VERSION AV714044.1 GI:10795561

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 626)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
 Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
 Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
 Lu,G., Cheng,Z. and Han,Z.

Homo sapiens cDNA DCB clones

Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

Location/Qualifiers

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1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBCHF06"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_lib="DCS"
/note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"

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ORIGIN

Query Match 25.4%; Score 564.2; DB 9; Length 626;
 Best Local Similarity 99.5%; Pred. No. 1.4e-72;

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Matches 566; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 61 ATAACTTTTATTTCTACTATGTATATGATGAAATGATTAATAAATGAACTAGCGAAG 120
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Db 58 ATAACTTTTATTTCTACTATGTATATGATGAAATGATTAATAAATGAACTAGCGAAG 117
|||||
Qy 121 GATGTAATAAATAGACATCTCTTTCATTTTACAGAGAGATGAAACAACTGCTTTTC 180
|||||
Db 118 GATGTAATAAATAGACATCTCTTTCATTTTACAGAGAGATGAAACAACTGCTTTTC 177
|||||
Qy 181 TTTTCTCAATTAATATGTGTGAATCAAGAGAAAACCTTTTTCAGAGTTAATACATGGT 240
|||||
Db 178 TTTTCTCAATTAATATGTGTGAATCAAGAGAAAACCTTTTTCAGAGTTAATACATGGT 237
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Qy 241 TCAGGAAAAGAGAAACCAAGCAAGCAAGCCAAATCAGAGCTAAGGAAAAGAAATAGA 300
|||||
Db 238 TCAGGAAAAGAGAAACCAAGCAAGCAAGCCAAATCAGAGCTAAGGAAAAGAAATAGA 297
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Qy 301 CTAAGTCTTCTGTGCAGAAACCTGAGTTTCATGAAGACACCCGCTCCAGTAGATCTGGG 360
|||||
Db 298 CTAAGTCTTCTGTGCAGAAACCTGAGTTTCATGAAGACACCCGCTCCAGTAGATCTGGG 357
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Qy 361 CACTTGGCCAAAGAAACCAAGAGTCTCCCTCGAAGAGCAGTGAAATGGGGTGAATCATTT 420
|||||
Db 358 CACTTGGCCAAAGAAACCAAGAGTCTCCCTCGAAGAGCAGTGAAATGGGGTGAATCATTT 417
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Qy 421 GACAACTGCTTTCCCATAGAGTGGCTAGAGGCTTTTACCAGATTTCTTAAACTGAA 480
|||||
Db 418 GACAACTGCTTTCCCATAGAGTGGCTAGAGGCTTTTACCAGATTTCTTAAACTGAA 477
|||||
Qy 481 TTCAGTGAAGAAATATTCAAATTTTGGATAGCTGTGAAGATTTCAAGAAAAGCAAGGGA 540
|||||
Db 478 TTCAGTGAAGAAATATTCAAATTTTGGATAGCTGTGAAGATTTCAAGAAAAGCAAGGGA 537
|||||
Qy 541 CTTCAACAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGACTGATGCC 600
|||||
Db 538 CTTCAACAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGACTGATGCC 597
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Qy 601 CCAAAAGAGGTTAACTTGAATTTTCACAC 629
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Db 598 CCAAAAGAGGTTAACTTGAATTTTCACAC 626

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RESULT 13

CF181629 723 bp mRNA linear EST 28-JUL-2003
 LOCUS 818478 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION CF181629

VERSION CF181629.1 GI:33293405

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1. (bases 1 to 723)

Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,

Wise,T.A., Nommman,D.J., Wray,J.E. and Keele,J.W.

A second set of porcine ESTs from a pooled-tissue normalized

library

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.

Plate: SRG8012 row: O column: 18

Seq primer: GTAATACGACTCACTATAGGG.

Location/Qualifiers

1..723

FEATURES

source

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Equus caballus (horse)	Equus caballus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.	1 (bases 1 to 661)	Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Moore, J. N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L. H.	An EST database from equine (Equus caballus) unstimulated peripheral blood leukocytes	Unpublished (2003)
Other ESTs: Leukon2_8 B10.b2_A024	Contact: Cordonnier-Pratt MM	Laboratory for Genomics and Bioinformatics	The University of Georgia, Department of Plant Biology	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA	Tel: 706 542 1860	Fax: 706 583 0210
Email: mmpratt@uga.edu	Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.	Seq primer: Sug5 (CTTGTGCTCTAAAGACTGCG)	Location/Qualifiers			
source						
1..661	/organism="Equus caballus"	/mol_type="mRNA"	/strain="thoroughbred"	/db_xref="taxon:9796"	/clone="Leukon2_8_B10_A024"	/sex="male"
	/tissue_type="blood"	/cell_type="leukocytes"	/lab_host="DH10B-R1 phage-resistant E. coli"	/clone_lib="Unstimulated peripheral blood leukocytes N2"	/note="Organ: circulatory system; Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from unstimulated equine peripheral blood leukocytes isolated from a healthy adult horse. Double-stranded cDNA was cloned unidirectionally into different draiii sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTG). XhoI excises the cDNA insert."	
ORIGIN						
Query Match	24.8%;	Score 550;	DB 14;	Length 661;		
Best Local Similarity	90.6%;	Pred: No. 1.6e-70;	Mismatches 0;	Indels 2;	Gaps 1;	
Matches 598;	Conservative					
QY	121	GATGTAATAAATTAGACATCTCTTCATTTTAGAG--AGAAGATGGAACACATGCTTT	178			
Db	2	GGTGTAAATAATTAGACGCTCTCTTCATTTTAGAGAAAGAGATGGAACATGCTTT	61			
QY	179	TCTTTTCTCAATAATATGTGTGAATCAAAAGAAAACCTTTTTCAGAGTTAATACATG	238			
Db	62	TCTTTTCTCAATAATATGTGTGAATCAAAAGAAAACCTTTTTCAGAGTTAATACATG	121			
QY	239	GTTTCAGAAAAGAAAACAAGCAAGAAAGCCAAATCAGAGCTTAAGGAAAAAATA	298			
Db	122	GTTTCAGAAAAGAAAACAAGCAAGAAAGCCAAATCAGAGCTTAAGGAAAAAATA	181			
QY	299	GACTAAGTCTTCTGTGAGAAACCTGAGTTTCATGAGACACCGCTCCAGTAGATCTG	358			
Db	182	GGTTAAGTCTGCTCTGTGAGAAACCTGAGTTTCATGAGACACCGCTCCAGTAGATCTG	241			
QY	359	GGCAGCTTGCCAAAAGAAAACAAGAGTCTCCCTCGAAGCGCAGTGAATATGGGCTGAATCAT	418			
Db	242	GGCAGCTTGCCAAAAGAAAACAAGAGTCTCCCTCGAAGCGCAGTGAATATGGGCTGAATCAT	301			

QY 419 TTGACAAACTGCTTTCCCATAGAGATGGACTAGAGGCTTTTACAGATTCTTAAACTG 478
 Db |||||
 QY 302 TTGACAAACTGCTTTCCCATAGAGATGGACTAGAGGCTTTTACAGATTCTTAAACTG 361
 Db |||||
 QY 479 AATTCAGTGAAGAAATATTGAATTTGGATAGCTGTGAGATTTCAGAAAGCAAGG 538
 Db |||||
 QY 362 AATTCAGTGAAGAAATATTGAATTTGGATAGCTGTGAGATTTCAGAAAGCAAGG 421
 Db |||||
 QY 539 GACCTCAACAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGACTGATG 598
 Db |||||
 QY 422 ACCCTCAACAATTTATCCTTAAAGCAAGCAATATATGAGAAATTTATACAGACTGATG 481
 Db |||||
 QY 599 CCCAAAGAGGTTAACTTGAATTTTACACAAAGAGTCAATTAACAAGCATCACT 658
 Db |||||
 QY 482 CTCGCAAGAGGTTAACTTGAATTTTCCACCAAGAAATCAATTCGCAAGCATCACT 541
 Db |||||
 QY 659 AACCTACCTCCACAGTTTGTGATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAAG 718
 Db |||||
 QY 542 AACCCACTCTCACAGTTTGTGATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACAAG 601
 Db |||||
 QY 719 ACAGTTATACAGTTTCTGAAATCTGACATCTATTTAGACTTTGATGAAGGAAGACCTC 778
 Db |||||
 QY 602 ACAGTTATACAGTTTCTGAAATCTGACATCTATTTAGACTTTGACAGAGGAAGACCTC 661
 Db |||||

RESULT 15

AQ317367
 LOCUS 537 bp DNA linear GSS 04-MAY-1999
 DEFINITION RPC111-104A6.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-104A6,
 genomic survey sequence.

ACCESSION AQ317367

VERSION AQ317367.1 GI:4048618

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)

Adams M.D., Rounsley S.D., Zhao S., Bass S., Linher K., Golden K.,

Berry K., Granger D., Suh E., Wible C., de Jong P., and Venter J.C.

Use of human BAC End Sequences for Sequence-Ready Map Building

Unpublished (1998)

Other GSSs: RPC111-104A6.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPC1-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: SP6

Class: BAC ends.

FEATURES

Location/Qualifiers

1..537

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="GDB:7539557"

/db_xref="taxon:9606"

/clone="RPC1-11-104A6"

/sex="Male"

/cell_type="Lymphocytes"

/clone_lib="RPC1-11"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

RPC111 Human Male BAC Library"

ORIGIN

Query Match 24.2%; Score 537; DB 28; Length 537;

Best Local Similarity 100.0%; Pred. No. 1.4e-68;
 Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 829 TTCCAAGATGTAACAATCAGATGTTGCCATTTGGTTATARAAGAAATGATTTTGTCTATT 888
 Db |||||
 QY 1 TTCCAAGATGTAACAATCAGATGTTGCCATTTGGTTATARAAGAAATGATTTTGTCTATT 60
 Db |||||
 QY 889 TTTATGACAAACTTTATACATCTGCTTCTAACATATCGCATGTTTATGTTTAAAGATTGGTC 948
 Db |||||
 QY 61 TTTATGACAAACTTTATACATCTGCTTCTAACATATCGCATGTTTATGTTTAAAGATTGGTC 120
 Db |||||
 QY 949 CAACTCTTTAAACTGAAATATGTCATGCAAAATTAATTTTAAATAATGTAATAAACAATTT 1008
 Db |||||
 QY 121 CCACTCTTTAAACTGAAATATGTCATGCAAAATTAATTTTAAATAATGTAATAAACAATTT 180
 Db |||||
 QY 1009 TCTGCTTAAACAAATACATACAGTATCTGCCAGTATATCTGTAAACCTTCTTATTGATG 1068
 Db |||||
 QY 181 TCTGCTTAAACAAATACATACAGTATCTGCCAGTATATCTGTAAACCTTCTTATTGATG 240
 Db |||||
 QY 1069 TCATTCCTTTTAAATCAAGAAAAAACTTATTTCTTAATCAAAAGGCGAGTACAAAAAA 1128
 Db |||||
 QY 241 TCATTCCTTTTAAATCAAGAAAAAACTTATTTCTTAATCAAAAGGCGAGTACAAAAAA 300
 Db |||||
 QY 1129 GTAATAATGTTTTATAAGATTGTAGAGTTAAGTAAAGTTAAGCTTTTGCRAAGTTGTCA 1188
 Db |||||
 QY 301 GTAATAATGTTTTATAAGATTGTAGAGTTAAGTAAAGTTAAGCTTTTGCRAAGTTGTCA 360
 Db |||||
 QY 1189 AAAGTTCAAAACAAAGTCTAGTTGGGATTTTACCAGAGCAGCATAATATGTTTATAT 1248
 Db |||||
 QY 361 AAAGTTCAAAACAAAGTCTAGTTGGGATTTTACCAGAGCAGCATAATATGTTTATAT 420
 Db |||||
 QY 1249 AACATATAATACTACTCAGATATCCAAATGTTTCAGATAGCATTTCATAATGAATTTCT 1308
 Db |||||
 QY 421 AACATATAATACTACTCAGATATCCAAATGTTTCAGATAGCATTTCATAATGAATTTCT 480
 Db |||||
 QY 1309 CTTTTTTTGGTAATAGTGTAGAAGTGTCTGGTTCTTACATGGGAGATGAAGAAC 1365
 Db |||||
 QY 481 CTTTTTTTGGTAATAGTGTAGAAGTGTCTGGTTCTTACATGGGAGATGAAGAAC 537
 Db |||||

Search completed: August 20, 2004, 12:31:50

Job time : 6017.98 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      August 20, 2004, 12:36:30 ; Search time 79 Seconds
              (without alignments)
              840.489 Million cell updates/sec

Title:        US-09-894-749-2
Perfect score: 1218
Sequence:     1 MTTTLFFSQINMCSEKKT.....SRSTCFNEFDQSDVAIL 235

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:    1585107 seqs, 282547505 residues

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1218	100.0	235	3	AA97153	AA97153	Human reg
2	1218	100.0	235	5	AA625829	AA625829	Human reg
3	1218	100.0	235	5	AAU10749	AAU10749	Human RGS
4	1218	100.0	235	5	ABP64801	ABP64801	Human pro
5	1176	96.6	227	5	ABP64054	ABP64054	Human ORF
6	1032	84.7	235	3	AA971754	AA971754	Murine re
7	1032	84.7	235	5	AA625830	AA625830	Murine re
8	422.5	34.7	211	6	ABP96779	ABP96779	Human COP
9	422.5	34.7	211	6	ABP98020	ABP98020	Amino aci
10	422.5	34.7	211	7	ADD14019	ADD14019	Human src
11	422.5	34.7	220	3	AA656929	AA656929	Human pro
12	421.5	34.6	181	2	AA462075	AA462075	Human reg
13	421.5	34.6	181	3	AA953931	AA953931	A human r
14	421.5	34.6	190	5	ABP62144	ABP62144	Human sec
15	413	33.9	81	5	AAU10747	AAU10747	Amino aci
16	410.5	33.7	181	5	ABB83788	ABB83788	Rat disea
17	409	33.6	930	6	ABB99465	ABB99465	Amino aci
18	408.5	33.5	205	5	AAU78976	AAU78976	Human RGS
19	408.5	33.5	205	7	AD622388	AD622388	Human Pro
20	408.5	33.5	205	7	AD623392	AD623392	Human Pro
21	405	33.3	188	4	AA622187	AA622187	Human RGS
22	404.5	33.2	205	7	AD622386	AD622386	Rat Prote
23	404.5	33.2	205	7	AD622390	AD622390	Rat Prote
24	404	33.2	519	4	AA930786	AA930786	Human she
25	404	33.2	519	6	ABB99466	ABB99466	Amino aci

CC present sequence represents the RGS18 polypeptide isolated from human platelets

XX Query Match 100.0%; Score 1218; DB 5; Length 235;

SQ Best Local Similarity 100.0%; Pred. No. 3.5e-111; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTLLFFSQINMCSEKTEFFKLHSGSGKEETSKEAKIRAKENRNLNLLVQKPEFHED 60

DB 1 METTLLFFSQINMCSEKTEFFKLHSGSGKEETSKEAKIRAKENRNLNLLVQKPEFHED 60

QY 61 TRSSRSGHLAKETRVSPPEAVKMGESFDKLLSHRDGLEAFTRFLKTEFSEENIEFWIACE 120

DB 61 TRSSRSGHLAKETRVSPPEAVKMGESFDKLLSHRDGLEAFTRFLKTEFSEENIEFWIACE 120

QY 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDFHTKEVITNSITQPTLHSPDAAQSRV 180

DB 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDFHTKEVITNSITQPTLHSPDAAQSRV 180

QY 181 YQLEQDSYTRFLKSDIYLDLMEGRPQRTNLRSSRSFTCNFQDVQSDVAIWL 235

DB 181 YQLEQDSYTRFLKSDIYLDLMEGRPQRTNLRSSRSFTCNFQDVQSDVAIWL 235

RESULT 4

ABP64801 ID ABP64801 standard; protein; 235 AA.

AC ABP64801;

XX 25-FEB-2003 (first entry)

DT Human protein SEQ ID 461.

DE

XX Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; neutropenic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective.

OS Homo sapiens.

XX WO200259260-A2.

PN 01-AUG-2002.

XX 16-NOV-2001; 2001WO-US042950.

PF 17-NOV-2000; 2000US-00714936.

PR (HYSE-) HYSEQ INC.

XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao Qa;

PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX WPI; 2002-590824/63.

DR N-PSDB; ABQ9387.

XX New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.

PS Claim 20; SEQ ID NO 461; 394pp; English.

XX The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABP6482-ABP65022). The sequences are useful in therapeutic, diagnostic and research methods. The polynucleotides may be used in the field of molecular biology as hybridisation probes, primers

CC present sequence represents the RGS18 polypeptide isolated from human platelets

XX Query Match 100.0%; Score 1218; DB 5; Length 235;

SQ Best Local Similarity 100.0%; Pred. No. 3.5e-111; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METTLLFFSQINMCSEKTEFFKLHSGSGKEETSKEAKIRAKENRNLNLLVQKPEFHED 60

DB 1 METTLLFFSQINMCSEKTEFFKLHSGSGKEETSKEAKIRAKENRNLNLLVQKPEFHED 60

QY 61 TRSSRSGHLAKETRVSPPEAVKMGESFDKLLSHRDGLEAFTRFLKTEFSEENIEFWIACE 120

DB 61 TRSSRSGHLAKETRVSPPEAVKMGESFDKLLSHRDGLEAFTRFLKTEFSEENIEFWIACE 120

QY 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDFHTKEVITNSITQPTLHSPDAAQSRV 180

DB 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDFHTKEVITNSITQPTLHSPDAAQSRV 180

QY 181 YQLEQDSYTRFLKSDIYLDLMEGRPQRTNLRSSRSFTCNFQDVQSDVAIWL 235

DB 181 YQLEQDSYTRFLKSDIYLDLMEGRPQRTNLRSSRSFTCNFQDVQSDVAIWL 235

RESULT 3

AAU10749 ID AAU10749 standard; protein; 235 AA.

AC AAU10749;

XX 12-MAR-2002 (first entry)

DT Human RGS18 polypeptide.

DE

XX Human; regulator of G protein signalling; RGS18; arterial thrombosis; platelet activation dysfunction; myocardial infarction; stroke; coronary artery disease; cerebrovascular disease; unstable angina; deep vein thrombosis; systemic thromboembolism; anti-coagulant; invasive cardiac procedure.

OS Homo sapiens.

XX WO200183514-A2.

PN 08-NOV-2001.

XX 26-APR-2001; 2001WO-US013540.

PF 28-APR-2000; 2000US-0200786P.

PR 02-AUG-2000; 2000GB-00018833.

XX (AVET) AVENTIS PHARM PROD INC.

XX Murray DL, Gagnon AW;

XX WPI; 2002-055453/07.

DR N-PSDB; AAS18340.

XX Isolated regulator of G protein signalling polypeptide, useful for prevention/treatment of platelet activation dysfunction, such as arterial thrombosis, myocardial infarction, coronary artery disease and stroke.

PS Claim 31; Fig 1; 127pp; English.

XX The present invention relates to the isolation of polynucleotide sequences, that encode a novel regulator of G protein signalling (RGS) polypeptide, RGS18, from human platelets. The invention also provides nucleotide primers and probes specific for an RGS18 nucleic acid. The sequences of the invention are useful for the manufacture of a medicament for the prevention or treatment of a platelet activation dysfunction, such as arterial thrombosis, myocardial infarction, coronary artery disease, stroke, cerebrovascular disease, unstable angina, deep vein thrombosis, systemic thromboembolism, and in invasive cardiac procedures for anti-coagulant purposes. The sequences of the invention can also be used for the detection of RGS18 nucleic acids and RGS18 polypeptides. The

CC for PCR, for chromosome and gene mapping, for the recombinant production
 CC of protein, or in generation of anti-sense DNA or RNA. The
 CC polynucleotides are useful in diagnostics as expressed sequence tags
 CC (ESTs) for identifying expressed genes or for physical mapping of the
 CC human genome. The proteins may be used as molecular weight markers, or as
 CC nutritional sources or supplements. The proteins may be used to maintain
 CC and expand cell population in a totipotential or pluripotential state
 CC useful for re-engineering damaged or diseased tissues, transplantation,
 CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
 CC polynucleotides and proteins are useful for preventing, treating or
 CC ameliorating disorders involving aberrant protein expression or
 CC biological activity, e.g. haematopoietic disorders, central/peripheral
 CC nervous system diseases, mechanical and traumatic disorders, non-healing
 CC wounds, immune deficiencies and disorders, infectious diseases caused by
 CC viral, bacterial or fungal infection, autoimmune disorders, allergic
 CC reactions and conditions, coagulation disorders, or cancer. The
 CC polynucleotide sequences of the invention were assembled from ESTs
 CC isolated mainly by sequencing by hybridisation, and in some cases,
 CC sequences obtained from one or more public databases. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 235 AA;

Query Match 100.0%; Score 1218; DB 5; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.5e-111; Indels 0; Gaps 0;
 Matches 235; Conservative 0; Mismatches 0;
 QY 1 METTLFFSQINNCSEKTEFFKLHGSGKETSKEAKIRAKENRSLLVQKEPHEH 60
 DB 1 METTLFFSQINNCSEKTEFFKLHGSGKETSKEAKIRAKENRSLLVQKEPHEH 60
 QY 61 TRSSRSGHLAKETRVSPPEAVKWSGDFKLHSHRDGLEAFTFLKTEPSEENIEFWIACE 120
 DB 61 TRSSRSGHLAKETRVSPPEAVKWSGDFKLHSHRDGLEAFTFLKTEPSEENIEFWIACE 120
 QY 121 DPKKSGPQOIHLKAKAIYEKFIQTDAPKEVNDPHTKEVITNSITQPTLHSDFAAQSRV 180
 DB 121 DPKKSGPQOIHLKAKAIYEKFIQTDAPKEVNDPHTKEVITNSITQPTLHSDFAAQSRV 180
 QY 181 YQMEQDSYTRFLKSDIYLDLMMEGRPQPTNLRRSRSTFCNEFDVQSDVAIWL 235
 DB 181 YQMEQDSYTRFLKSDIYLDLMMEGRPQPTNLRRSRSTFCNEFDVQSDVAIWL 235

RESULT 5
 ID ABP64054 standard; protein; 227 AA.
 XX ABP64054;
 AC ABP64054;
 DT 04-NOV-2002 (first entry)
 DE Human ORP424.
 XX Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary;
 XX Antinflammatory; gene therapy; human; ORFX; atherogenic; platelet;
 XX human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;
 XX cancer; cardiovascular disease; allergy; autoimmune disease;
 XX wound healing; blood coagulation disorder; inflammatory disorder.
 XX Homo sapiens.
 OS
 XX US2002082206-A1.
 XX 27-JUN-2002.
 XX 30-MAY-2001; 2001US-00867550.
 XX 30-MAY-2000; 2000US-0208427P.
 XX (LEAC/) LEACH M D.

FA (MEHR/) MEHRABAN F.
 PA (CONL/) CONLEY P B.
 PA (TOPP/) TOPPER J N.
 PA (LAWD/) LAW D.
 XX
 PI Leach MD, Mehraban F, Conley PB, Topper JN, Law D;
 DR WPI; 2002-626554/67.
 DR N-PSDB; ABQ98617.
 XX
 PT New polypeptide designated ORFX are present in human atherogenic cells
 PT and are useful to prevent and treat ORFX-associated disorders including
 PT cancer, allergy, wound healing or autoimmune, cardiovascular or
 PT inflammatory disease.
 XX
 PS Claim 10; SEQ ID NO 848; 78pp; English.
 XX
 CC The present invention relates to novel human ORFX polypeptides and their
 CC coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences
 CC were discovered in human atherogenic cells, in particular in platelets
 CC and human umbilical vein endothelial cells (HUVEC) and are expressed in
 CC many other tissues as well. Atherogenic cells are cells which have the
 CC potential to develop atherosclerotic plaques. The ORFX polypeptides and
 CC nucleic acids are useful for treating or preventing a pathological
 CC condition associated with an ORFX-associated disorder, e.g. cancer,
 CC cardiovascular disease, allergy, autoimmune disease, wound healing, blood
 CC coagulation disorders or inflammatory disorders. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from the USPTO web site at
 CC segdata.uspto.gov/sequence.html?DocID=20020082206
 XX
 SQ Sequence 227 AA;

Query Match 96.6%; Score 1176; DB 5; Length 227;
 Best Local Similarity 100.0%; Pred. No. 4.5e-107; Indels 0; Gaps 0;
 Matches 227; Conservative 0; Mismatches 0;
 QY 1 METTLFFSQINNCSEKTEFFKLHGSGKETSKEAKIRAKENRSLLVQKEPHEH 60
 DB 1 METTLFFSQINNCSEKTEFFKLHGSGKETSKEAKIRAKENRSLLVQKEPHEH 60
 QY 61 TRSSRSGHLAKETRVSPPEAVKWSGDFKLHSHRDGLEAFTFLKTEPSEENIEFWIACE 120
 DB 61 TRSSRSGHLAKETRVSPPEAVKWSGDFKLHSHRDGLEAFTFLKTEPSEENIEFWIACE 120
 QY 121 DPKKSGPQOIHLKAKAIYEKFIQTDAPKEVNDPHTKEVITNSITQPTLHSDFAAQSRV 180
 DB 121 DPKKSGPQOIHLKAKAIYEKFIQTDAPKEVNDPHTKEVITNSITQPTLHSDFAAQSRV 180
 QY 181 YQMEQDSYTRFLKSDIYLDLMMEGRPQPTNLRRSRSTFCNEFDV 227
 DB 181 YQMEQDSYTRFLKSDIYLDLMMEGRPQPTNLRRSRSTFCNEFDV 227

RESULT 6
 ID AAY97154 standard; protein; 235 AA.
 XX AAY97154;
 AC AAY97154;
 DT 04-DEC-2000 (first entry)
 XX Murine regulator of G-protein signaling protein.
 DE
 XX RGS; regulators of G-protein signaling; GTPase activating protein; GAP;
 XX G-alpha protein; cell adhesion; chemotaxis; vulnerary; immunosuppressor;
 XX anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
 XX cytostatic; hepatotropic; anti-anemic; modulator; gene therapy.
 XX Mus sp.
 XX Key
 XX Location/Qualifiers
 FT Domain 82..201

FT Misc-difference 83 /label= RGS_domain
 FT /note= "forms part of hydrophobic core"
 FT Misc-difference 90 /note= "forms part of hydrophobic core"
 FT Misc-difference 100 /note= "forms part of hydrophobic core"
 FT Misc-difference 103 /note= "forms part of hydrophobic core"
 FT Misc-difference 104 /note= "forms part of hydrophobic core"
 FT Misc-difference 107 /note= "forms part of hydrophobic core"
 FT Misc-difference 109 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 111 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 112 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 115 /note= "forms part of hydrophobic core"
 FT Misc-difference 116 /note= "forms part of hydrophobic core"
 FT Misc-difference 138 /note= "forms part of hydrophobic core"
 FT Misc-difference 139 /note= "forms part of hydrophobic core"
 FT Misc-difference 142 /note= "forms part of hydrophobic core"
 FT Misc-difference 143 /note= "forms part of hydrophobic core"
 FT Misc-difference 151 /note= "forms part of hydrophobic core"
 FT Misc-difference 152 /note= "forms part of hydrophobic core"
 FT Misc-difference 154 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 183 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 184 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 187 /note= "forms part of hydrophobic core"
 FT Misc-difference 188 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 189 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 191 /note= "forms part of hydrophobic core"
 FT Misc-difference 192 /note= "Makes direct contact with G-alpha-i"
 FT Misc-difference 193 /note= "forms part of hydrophobic core"
 FT Misc-difference 198 /note= "forms part of hydrophobic core"
 FT /note= "forms part of hydrophobic core"
 XX WO200046236-A2.
 XX 10-AUG-2000.
 XX 04-FEB-2000; 2000WO-US002977.
 XX 04-FEB-1999; 99US-00244314.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Hodge MR, Yowe D;
 XX WPI; 2000-532893/48.
 XX N-PSDB; AAA52090.
 XX Novel regulator of G-protein signaling nucleic acids and polypeptides,
 XX useful as diagnostic and investigative tools and to treat G-protein

PT signaling disorders.

XX Claim 8; Page 104; 105pp; English.

XX The RGS (regulators of G-protein signaling) protein genes, clones
 CC AAH16395 and m1975, were identified in human and murine spleen cDNA
 CC libraries, respectively. Both proteins have unique N- and C-terminal
 CC sequences. The C-terminal location of the RGS domain is consistent with
 CC RGS known to act as GTPase activating proteins (GAPs) for G-alpha
 CC proteins. G-alpha-1 linked receptors support rapid adhesion and directed
 CC migration of leukocytes and other cell types. The novel RGS proteins may
 CC be used to modulate cell adhesion and chemotaxis, e.g. for aiding wound
 CC repair. The RGS proteins, related cDNAs and anti-RGS antibodies are
 CC useful for modulation, diagnosis and treatment of immune and respiratory
 CC disorders

XX Sequence 235 AA;

Query Match 84.7%; Score 1032; DB 3; Length 235;
 Best Local Similarity 83.8%; Pred. No. 6.6e-93;
 Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 METTLLPFGQINMCSEKXTFFKLHGSGKETSKEAKIRAKENRLSLVQKPEFHED 60

DB 1 MDMSLVFFSQLNMCSEKXTFFKLHGSGKETSKEAKIRAKENRLSLVQKPEFHED 60

QY 61 TRSSRSCHLAKETRVSPPEAVKWSGFDKLLSHRDGLAFTFLKTEFSEENIEFWACE 120

DB 61 TQASRSALLAKETRVSPPEAVKWSGFDKLLSHRDGLAFTFLKTEFSEENIEFWACE 120

QY 121 DFKKSGPQOIHLKAKIYEKFIQTADAPKEVNLDPHTKEVITNSITQPTLHSPDAQSRV 180

DB 121 DFKKCKEPOQIILKAKIYEKFIQTADAPKEVNLDPHTKEVITNSITQPTLHSPDAQSRV 180

QY 181 YQMEODSYTRFLKSDIYLDLMGRPQPTNLRSSRSFTCNCFQVQSDVAIWL 235

DB 181 YQMEHDSYRFLKSELYLHLIEGRPQPTNLRSSRSFTCNCFQVQSDVAIWL 235

RESULT 7

AAE25830

ID AAE25830 standard; protein; 235 AA.

XX AAE25830;

DT 15-NOV-2002 (first entry)

XX Murine regulator of G-protein signalling (RGS) protein, m1975.

XX Murine; screening; RGS; regulator of G-protein signalling; pancreatitis;
 KW inflammatory disorder; allergy; Grave's disease; arthritis; sinusitis;
 KW respiratory disorder; asthma; pneumonia; therapy; immune disorder;
 KW haematological disorder; haematopoiesis; platelet-associated disorder;
 KW thrombocytopaenia; migration; invasive disorder; leukaemia; anaemia;
 KW erythrocyte-associated disorder; hepatitis; m1975.

XX Mus sp.

XX Key Location/Qualifiers
 FT Domain 82..201
 FT /note= "RGS domain"

XX US6410240-B1.

XX 25-JUN-2002.

XX 04-FEB-2000; 2000US-00498959.

XX 04-FEB-1999; 99US-00244314.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hodge MR, Yowe D;

PN WO9958670-A1.
 XX 18-NOV-1999.
 PD 07-MAY-1999; 99WO-US010151.
 XX 08-MAY-1998; 98US-0084842P.
 PF 07-OCT-1998; 98US-0103355P.
 XX (CADU-) CADUS PHARM CORP.
 PA Cismowski M, Duzic E;
 PI WPI; 2000-072337/06.
 DR N-PSDB; AAZ36910.
 XX A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity.
 XX Claim 74; Page 141-141; 162pp; English.
 XX The present sequence represents a regulator of G protein signalling (AGS)
 CC protein, RGS5. The specification also describes an activator of G protein
 CC signalling (AGS) protein. The AGS cDNA sequence was isolated from a human
 CC liver cDNA library. The AGS protein exhibits homology to ras-related G
 CC proteins, and contains alterations in conserved amino acids consistent
 CC with a deficiency in GTP hydrolysis activity. AGS stimulates G protein
 CC activity, G protein-coupled signal transduction and the pheromone
 CC response pathway in a receptor-independent manner. The AGS protein also
 CC shows G-gamma selectivity, as measured by growth assays in yeast
 CC expressing various mammalian G-gamma constructs, and tissue-specific
 CC expression, as measured by Northern blot analysis. The AGS protein can be
 CC used to screen for compounds that modulate cellular signal transduction.
 CC The protein is used to treat disorders characterized by an aberrant AGS
 CC protein activity or AGS nucleic acid expression
 XX Sequence 181 AA;
 SQ
 Query Match 34.6%; Score 421.5; DB 3; Length 181;
 Best Local Similarity 49.1%; Pred. No. 4.3e-33;
 Matches 82; Conservative 37; Mismatches 45; Indels 3; Gaps 1;
 QY 40 RAKEKRNRLSLVQKPEFHED---TRSSRSHLAKETRVSPPEAVKMGESFDKLLSHRDG 96
 DB 15 RAKEIKIKGILLQKPDVGLVPIYNEKPEPAKTOKTSLDEALQWDSLDKLLQNNYG 74
 QY 97 LEAFTRLFKTEFSEENIEFWIACEDFKKSGPQOIHAKAIYKFIOTDAPKEVNLDFH 156
 DB 75 LASFKSFLKSEFSEENLEFWIACEDYKKIKSPAKMAEKAKQIYEFYQTEAPKEVNDHF 134
 QY 157 TKEVITNSITOPTLHSPDAQSRVYQVLMQDSYTRFLKSDIYLDLME 203
 DB 135 TKDITMKNLVEPSLSFDMQAKRIHALMEKDSLPRFVRSEFYQELIK 181
 RESULT 14
 ABP62144
 ID ABP62144 standard, protein; 190 AA.
 XX ABP62144;
 AC
 XX 12-NOV-2002 (first entry)
 DT
 XX Human secreted protein SEQ ID NO 197.
 DE
 XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnary;
 KW antiparkinsonian; antisticking; antianaemic; antiinflammatory; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antitumor; antiallergic;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
 XX

OS Homo sapiens.
 XX WO200257420-A2.
 PN 25-JUL-2002.
 PD 17-JAN-2002; 2002WO-US001109.
 XX 18-JAN-2001; 2001US-0262066P.
 PF (HUMA-) HUMAN GENOME SCI INC.
 XX Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen CA, Olsen H;
 PI Ebner R, Brewer LA;
 XX WPI; 2002-599716/64.
 DR New polynucleotides and polypeptides useful for diagnosing, prognosing,
 XX treating or preventing e.g. neurodegenerative, central nervous system,
 PT autoimmune, respiratory, reproductive, or inflammatory diseases or
 PT disorders.
 XX Claim 11; Page 71; 785pp; English.
 PS The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
 CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections
 XX Sequence 190 AA;
 SQ
 Query Match 34.6%; Score 421.5; DB 5; Length 190;
 Best Local Similarity 49.1%; Pred. No. 4.6e-33;
 Matches 82; Conservative 37; Mismatches 45; Indels 3; Gaps 1;
 QY 40 RAKEKRNRLSLVQKPEFHED---TRSSRSHLAKETRVSPPEAVKMGESFDKLLSHRDG 96
 DB 24 RAKEIKIKGILLQKPDVGLVPIYNEKPEPAKTOKTSLDEALQWDSLDKLLQNNYG 83
 QY 97 LEAFTRLFKTEFSEENIEFWIACEDFKKSGPQOIHAKAIYKFIOTDAPKEVNLDFH 156
 DB 84 LASFKSFLKSEFSEENLEFWIACEDYKKIKSPAKMAEKAKQIYEFYQTEAPKEVNDHF 143
 QY 157 TKEVITNSITOPTLHSPDAQSRVYQVLMQDSYTRFLKSDIYLDLME 203
 DB 144 TKDITMKNLVEPSLSFDMQAKRIHALMEKDSLPRFVRSEFYQELIK 190
 RESULT 15
 AAU10747
 ID AAU10747 standard; protein; 81 AA.
 XX AAU10747;
 AC
 XX 12-MAR-2002 (first entry)
 DT
 XX Amino acid sequence of partial human platelet RGS domain.
 DE
 XX Human; regulator of G protein signalling; RGS18; arterial thrombosis;
 KW platelet activation dysfunction; myocardial infarction; stroke;
 KW coronary artery disease; cerebrovascular disease; unstable angina;
 KW deep vein thrombosis; systemic thromboembolism; anti-coagulant;
 XX

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OM protein - protein search, using sw model

Run on: August 20, 2004, 16:40:58 ; Search time 18.5 Seconds
(without alignments)
655.789 Million cell updates/sec

Title: US-09-894-749-2

Perfect score: 1218

Sequence: 1 METTLFFSQINNCESKKT.....SRSTFCNEFQVQSDVAIWL 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1218	100.0	235	3	US-09-244-314-2
2	1218	100.0	235	4	US-09-498-959-2
3	1032	84.7	235	3	US-09-244-314-4
4	1032	84.7	235	4	US-09-498-959-4
5	422.5	34.7	211	2	US-08-748-483-4
6	421.5	34.6	181	2	US-08-748-483-1
7	408.5	33.5	205	2	US-08-829-110-6
8	408.5	33.5	205	2	US-08-748-483-5
9	380	31.2	202	1	US-08-274-318-2
10	380	31.2	202	2	US-08-463-081B-2
11	380	31.2	202	2	US-08-461-379A-2
12	380	31.2	202	2	US-08-462-390B-2
13	380	31.2	202	2	US-08-754-108-2
14	380	31.2	202	3	US-08-870-815-4
15	380	31.2	202	3	US-08-463-074B-2
16	380	31.2	202	3	US-08-465-585C-2
17	380	31.2	202	3	US-08-652-446-2
18	380	31.2	202	3	US-08-949-004-4
19	369	30.3	120	4	US-08-890-865A-11
20	361	29.6	201	2	US-08-726-228-2
21	361	29.6	201	3	US-08-870-815-2
22	361	29.6	201	3	US-08-949-004-2
23	359	29.5	120	4	US-08-890-865A-13
24	358.5	29.4	121	2	US-08-588-258B-32
25	358.5	29.4	121	3	US-08-460-505-32
26	358.5	29.4	121	5	PCT-US96-08295-32
27	358	29.4	120	4	US-08-890-865A-14

28	357	29.3	120	4	US-08-890-865A-12	Sequence 12, Appl
29	353	29.0	196	2	US-08-829-110-5	Sequence 5, Appli
30	353	29.0	196	2	US-08-748-483-3	Sequence 3, Appli
31	353	29.0	196	4	US-09-702-705-339	Sequence 339, App
32	353	29.0	196	4	US-09-736-457-339	Sequence 339, App
33	353	29.0	196	4	US-09-614-124B-339	Sequence 339, App
34	353	29.0	196	4	US-09-671-325-339	Sequence 339, App
35	353	29.0	196	4	US-09-589-184-339	Sequence 339, App
36	335.5	27.5	119	2	US-08-588-258B-31	Sequence 31, Appl
37	335.5	27.5	119	3	US-08-460-505-31	Sequence 31, Appl
38	335.5	27.5	119	5	PCT-US96-08295-31	Sequence 31, Appl
39	328.5	27.0	119	4	US-08-890-865A-15	Sequence 15, Appl
40	306	25.1	217	4	US-09-976-594-51	Sequence 51, Appl
41	290.5	23.9	119	2	US-08-588-258B-30	Sequence 30, Appl
42	290.5	23.9	119	3	US-08-460-505-30	Sequence 30, Appl
43	290.5	23.9	119	5	PCT-US96-08295-30	Sequence 30, Appl
44	287	23.6	159	2	US-08-829-110-1	Sequence 1, Appli
45	283	23.2	120	4	US-08-890-865A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-244-314-2

; Sequence 2, Application US/09244314

; Patent No. 6274362

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin R.

; APPLICANT: Yowe, David

; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof

; FILE REFERENCE: 5800-19, 035800/174680

; CURRENT APPLICATION NUMBER: US/09/244,314

; CURRENT FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 235

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-244-314-2

Query Match 100.0%; Score 1218; DB 3; Length 235;

Best Local Similarity 100.0%; Pred. No. 3.6e-116;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	METTLFFSQINNCESKKTFFKLIHSGKEETSKEAKIRAKERNRLSLLVQKPFHED	60
Db	1	METTLFFSQINNCESKKTFFKLIHSGKEETSKEAKIRAKERNRLSLLVQKPFHED	60
Qy	61	TRSRSGHLAKETRVSPPEAVKMGESFDKLLSHRDGLEAFTRELKTEFSEENIEFWIACE	120
Db	61	TRSRSGHLAKETRVSPPEAVKMGESFDKLLSHRDGLEAFTRELKTEFSEENIEFWIACE	120
Qy	121	DFKKSQPGQIHLKAKAIYEKFIQTDPKENVLDFTHTKEVITNSITQPTLHSPDAAQSRV	180
Db	121	DFKKSQPGQIHLKAKAIYEKFIQTDPKENVLDFTHTKEVITNSITQPTLHSPDAAQSRV	180
Qy	181	YQMEQDSYTRFLKSDIYLDLMGRQPTNLRSSRSTCTNEFQVQSDVAIWL	235
Db	181	YQMEQDSYTRFLKSDIYLDLMGRQPTNLRSSRSTCTNEFQVQSDVAIWL	235

RESULT 2

US-09-498-959-2

; Sequence 2, Application US/09498959

; Patent No. 6410240

; GENERAL INFORMATION:

; APPLICANT: Hodge, Martin R.

; APPLICANT: Yowe, David

; TITLE OF INVENTION: RGS-Containing Molecules and Uses

; TITLE OF INVENTION: Thereof

; FILE REFERENCE: 5800-19A

; CURRENT APPLICATION NUMBER: US/09/498,959
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: 09/244,314
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-498-959-2

Query Match 100.0%; Score 1218; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METTLFFSQINNCESKEKTFKLLHSGKETSKEAKIRAKENRSLVQKPEFHED 60
DB 1 METTLFFSQINNCESKEKTFKLLHSGKETSKEAKIRAKENRSLVQKPEFHED 60
QY 61 TRSSRSHLAKETRVSPEAVKWSGDFKLLSHRDGLAFTFLKTEFSEENIEFWACE 120
DB 61 TRSSRSHLAKETRVSPEAVKWSGDFKLLSHRDGLAFTFLKTEFSEENIEFWACE 120
QY 121 DFKKSGPQOIHLKAKAIYEKFIQDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQRV 180
DB 121 DFKKSGPQOIHLKAKAIYEKFIQDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQRV 180
QY 181 YOLMEODSVTRFKSDIYLDLMEGRPQPTNLRSSRSFTCNEFQDVQSDVAIWL 235
DB 181 YOLMEODSVTRFKSDIYLDLMEGRPQPTNLRSSRSFTCNEFQDVQSDVAIWL 235

RESULT 3

US-09-244-314-4
; Sequence 4, Application US/09244314
; Patent No. 6274362
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/244,314
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-244-314-4

Query Match 84.7%; Score 1032; DB 3; Length 235;
Best Local Similarity 83.8%; Pred. No. 3.2e-97;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
QY 1 METTLFFSQINNCESKEKTFKLLHSGKETSKEAKIRAKENRSLVQKPEFHED 60
DB 1 MDMSLVFFSQINNCESKEKTFKLLHSGKETSKEAKIRAKENRSLVQKPEFHED 60
QY 61 TRSSRSHLAKETRVSPEAVKWSGDFKLLSHRDGLAFTFLKTEFSEENIEFWACE 120
DB 61 TQASRALLAKETRVSPEAVKWSGDFKLLSHRDGLAFTFLKTEFSEENIEFWACE 120
QY 121 DFKKSGPQOIHLKAKAIYEKFIQDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQRV 180
DB 121 DFKKSGPQOIHLKAKAIYEKFIQDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQRV 180
QY 181 YOLMEODSVTRFKSDIYLDLMEGRPQPTNLRSSRSFTCNEFQDVQSDVAIWL 235
DB 181 YOLMEODSVTRFKSDIYLDLMEGRPQPTNLRSSRSFTCNEFQDVQSDVAIWL 235

RESULT 4

US-09-498-959-4
; Sequence 4, Application US/09498959
; Patent No. 6410240
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5800-19A
; CURRENT APPLICATION NUMBER: US/09/498,959
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: 09/244,314
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-498-959-4

Query Match 84.7%; Score 1032; DB 4; Length 235;
Best Local Similarity 83.8%; Pred. No. 3.2e-97;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
QY 1 METTLFFSQINNCESKEKTFKLLHSGKETSKEAKIRAKENRSLVQKPEFHED 60
DB 1 MDMSLVFFSQINNCESKEKTFKLLHSGKETSKEAKIRAKENRSLVQKPEFHED 60
QY 61 TRSSRSHLAKETRVSPEAVKWSGDFKLLSHRDGLAFTFLKTEFSEENIEFWACE 120
DB 61 TQASRALLAKETRVSPEAVKWSGDFKLLSHRDGLAFTFLKTEFSEENIEFWACE 120
QY 121 DFKKSGPQOIHLKAKAIYEKFIQDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQRV 180
DB 121 DFKKSGPQOIHLKAKAIYEKFIQDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQRV 180
QY 181 YOLMEODSVTRFKSDIYLDLMEGRPQPTNLRSSRSFTCNEFQDVQSDVAIWL 235
DB 181 YOLMEODSVTRFKSDIYLDLMEGRPQPTNLRSSRSFTCNEFQDVQSDVAIWL 235

RESULT 5

US-08-748-483-4
; Sequence 4, Application US/08748483
; Patent No. 5955314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Suriya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

```

; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0157 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 292037
; US-08-748-483-4

Query Match 34.7%; Score 422.5; DB 2; Length 211;
Best Local Similarity 42.8%; Pred. No. 3.4e-35;
Matches 89; Conservative 37; Mismatches 73; Indels 9; Gaps 3;

QY 6 LFFSOINNCESKEKTFKLIHSGKEETSKEAKIR--AKEKNRLSLLVQKPEFHEDTR 62
DB 5 MFLAVQHDCHRPMDKS-----AGSGHKSEKREKMTLLKQWKRLSYFLQNSSTPGKPK 59
QY 63 SSRSGHLAKETRVSPPEEAVKWGESFDKLLSHRDGLAEFTFLKTEFSEENIEFWIACEDF 122
DB 60 TGKSKQQAQFKPSPEEQLMSEAFDELLASKYGLAAAFRAFLKSEFCENIEFWLACEDF 119
QY 123 KSKGPQIHLKAKAIYEKFTQTDAPKEVNLDFHTKEVITNSITQPTLHSDAAQSRVYQ 182
DB 120 KTKSPQKLSKAKRIYTDIEKEAPKBEINIDFQTKLIAQIQEATSGCFTTAAKRVYS 179
QY 183 LMEODSYTRFLKSDIYLDLMEORPQPT 210
DB 180 LMENNSYPRFLESEYQDLCK-KPQIT 206

RESULT 6
US-08-748-483-1
; Sequence 1, Application US/08748483
; Patent No. 5955314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0157 US
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166

; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0157 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 57362
; US-08-748-483-1

Query Match 34.6%; Score 421.5; DB 2; Length 181;
Best Local Similarity 49.1%; Pred. No. 3.5e-35;
Matches 82; Conservative 37; Mismatches 45; Indels 3; Gaps 1;

QY 40 RAKEKNRLSLLVQKPEFHED---TRSSRSGHLAKETRVSPPEEAVKWGESFDKLLSHRDG 96
DB 15 RAXEIKIKGLILQKPDVGLVPIYNEKPEKPAKTQKTSLDPEALQWRDLSLKLQNNYG 74
QY 97 LEAFTFLKTEFSEENIEFWIACEDPKKSGKGPQIHLKAKAIYEKFTQTDAPKEVNLDPH 156
DB 75 LASFKFLKSEFSEENLEFWIACEDYKKIKSPAKMAEKAKQIYEFTQTEAPKEVNIHDF 134
QY 157 TKSVITNSITQPTLHSDAAQSRVYQLMEOQSYTRFLKSDIYLDLME 203
DB 135 TKDITMKNLVEPSLSLSDFAQKRIHALMEKDSLPRFVRSSEFYQELIK 181

RESULT 7
US-08-829-110-6
; Sequence 6, Application US/08829110
; Patent No. 5882890
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,110
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0259 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
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; CLONE: 1216373
; US-08-829-110-6

Query Match 33.5%; Score 408.5; DB 2; Length 205;
Best Local Similarity 49.1%; Pred. No. 8.8e-34;
Matches 82; Conservative 28; Mismatches 48; Indels 9; Gaps 2

QY 41 AKEKNRLSLLVQKPEFHEDTRSRSGHLAKE-----TRVSPPEAVKWGESFDKLLSHRD 95
Db 16 AXDMKRLGLFLQK-----SDCEHNSHNKKDKVVICQRVSQBEVKGWAESENLSHSEC 71
QY 96 GLEAFTRFKTEFSBENTEFWIACEDFKKSGKQPOIHLKAKAIYEKFIQTDAPKEVNLDF 155
Db 72 GLAFAKFAFKSFSYSENIDFWISEEYKIKSPKSLPKAKKLYNEFISVQATKEVNLDS 131
QY 156 HYKEVITNSITOPTUHSFDAQSRVYQLMQEDSYTRFKSDIYDLM 202
Db 132 CRTRETSRNLPEPTITCFDEAQKIFNLMEKDSYRFLKSRFYLDLV 178

RESULT 8
US-08-748-483-5
; Sequence 5, Application US/08748483
; Patent No. 5955314
; GENERAL INFORMATION:
; APPLICANT: Hallman, Jennifer L.
; APPLICANT: Geli, Surya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0157 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1216373
; US-08-748-483-5

Query Match 33.5%; Score 408.5; DB 2; Length 205;
Best Local Similarity 49.1%; Pred. No. 8.8e-34;
Matches 82; Conservative 28; Mismatches 48; Indels 9; Gaps 2

QY 41 AKEKNRLSLLVQKPEFHEDTRSRSGHLAKE-----TRVSPPEAVKWGESFDKLLSHRD 95

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Query Match 31.2%; Score 380; DB 3; Length 202;

Best Local Similarity 48.5%; Pred. No. 6.9e-31;
Matches 81; Conservative 28; Mismatches 52; Indels 6; Gaps 2;
QY 40 RAKEKRNLSLLVOKPEFHEDTRSS-----RSGHLAKETRVSPBEAVKVGESFDKLLSHR 94
DB 15 RAKEFKTRLGIFLHKSELGCDTGSTGKPEWGSKH-SKENRNFSDEVLGWRESFDLLLSK 73
QY 95 DGLEAFTFLKTEFSEENIEFWIACEDPKSKGPOQIHLKAKAIYKFIQTDAPKEVNLD 154
DB 74 NGVAAFHAFPLKTEFSEENIEFWIACEDPKSKGPOQIHLKAKAIYKFIQTDAPKEVNLD 133
QY 155 FHTKEVITNSITOPTLHSDFAAQSRVYQVLMQEDSYTRFLKSDIYLDL 201
DB 134 HETRELTRMNLQTATATCFDAAQKTRTLMKDSYPRFLKSPAYRDL 180

RESULT 15
US-08-463-074B-2
; Sequence 2, Application US/08463074B
; Patent No. 6020155
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; ADDRESS: (B) STREET:
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,074B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 202 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-074B-2

Query Match 31.2%; Score 380; DB 3; Length 202;
Best Local Similarity 48.5%; Pred. No. 6.9e-31;
Matches 81; Conservative 28; Mismatches 52; Indels 6; Gaps 2;
QY 40 RAKEKRNLSLLVOKPEFHEDTRSS-----RSGHLAKETRVSPBEAVKVGESFDKLLSHR 94
DB 15 RAKEFKTRLGIFLHKSELGCDTGSTGKPEWGSKH-SKENRNFSDEVLGWRESFDLLLSK 73
QY 95 DGLEAFTFLKTEFSEENIEFWIACEDPKSKGPOQIHLKAKAIYKFIQTDAPKEVNLD 154
DB 74 NGVAAFHAFPLKTEFSEENIEFWIACEDPKSKGPOQIHLKAKAIYKFIQTDAPKEVNLD 133

QY 155 FHTKEVITNSITOPTLHSDFAAQSRVYQVLMQEDSYTRFLKSDIYLDL 201
DB 134 HETRELTRMNLQTATATCFDAAQKTRTLMKDSYPRFLKSPAYRDL 180

Search completed: August 20, 2004, 16:48:32
Job time : 19.5 secs

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OM protein - protein search, using sw model

Run on: August 20, 2004, 16:47:08 ; Search time 239 Seconds

(without alignments)
308.996 Million cell updates/sec

Title: US-09-894-749-2

Perfect score: 1218

Sequence: 1 METLLFFSQINMCESKEKT.....SRSGTCNEFDQVSDVAIWL 235

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Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1032	84.7	235	9	US-09-894-749-4
5	422.5	34.7	211	9	US-09-206-639-4
6	422.5	34.7	211	12	US-10-258-371B-24
7	422.5	34.7	211	16	US-10-408-765A-493
8	422.5	34.7	220	9	US-09-925-300-1507
9	421.5	34.6	181	9	US-09-206-639-1
10	421.5	34.6	181	12	US-10-258-371B-22
11	421.5	34.6	190	14	US-10-411-224-197
12	421.5	34.6	190	15	US-10-047-021-197
13	413	33.9	181	12	US-10-258-371B-12
14	410.5	33.7	181	14	US-10-398-953-1
15	409	33.6	930	14	US-10-113-794A-1

16	408.5	33.5	205	9	US-09-206-639-5	Sequence 5, Appli
17	408.5	33.5	205	10	US-09-939-209A-2	Sequence 2, Appli
18	408.5	33.5	205	12	US-10-258-371B-21	Sequence 21, Appl
19	404	33.2	519	12	US-10-258-371B-28	Sequence 28, Appl
20	404	33.2	519	14	US-10-113-794A-2	Sequence 2, Appli
21	404	33.2	519	15	US-10-428-487-14	Sequence 14, Appl
22	404	33.2	591	15	US-10-108-260A-3970	Sequence 3970, Ap
23	402.5	33.0	180	12	US-10-258-371B-27	Sequence 27, Appli
24	402.5	33.0	180	14	US-10-275-555-2	Sequence 2, Appli
25	401	32.9	776	12	US-10-087-132-1728	Sequence 1728, Ap
26	400	32.8	284	15	US-10-094-749-1650	Sequence 1650, Ap
27	396.5	32.6	923	12	US-10-114-270-152	Sequence 152, App
28	380	31.2	202	9	US-09-873-438-4	Sequence 4, Appli
29	380	31.2	202	14	US-10-171-311-202	Sequence 202, App
30	380	31.2	204	12	US-10-258-371B-23	Sequence 23, Appl
31	370	30.4	128	15	US-10-352-843-1	Sequence 1, Appli
32	370	30.4	128	15	US-10-352-843-3	Sequence 3, Appli
33	370	30.4	167	10	US-09-942-055A-1	Sequence 1, Appli
34	361	29.6	69	12	US-10-258-371B-13	Sequence 13, Appli
35	361	29.6	201	9	US-09-873-438-2	Sequence 2, Appli
36	353	29.0	196	9	US-09-206-639-3	Sequence 3, Appli
37	353	29.0	196	9	US-09-736-457-339	Sequence 339, App
38	353	29.0	196	9	US-09-902-941-339	Sequence 339, App
39	353	29.0	196	9	US-09-849-626-339	Sequence 339, App
40	353	29.0	196	10	US-09-476-300-339	Sequence 339, App
41	353	29.0	196	12	US-10-283-017-339	Sequence 339, App
42	353	29.0	196	14	US-10-017-754-339	Sequence 339, App
43	353	29.0	196	14	US-10-113-872-339	Sequence 339, App
44	353	29.0	196	14	US-10-247-671-176	Sequence 176, App
45	353	29.0	217	9	US-09-925-301-1292	Sequence 1292, Ap

ALIGNMENTS

RESULT 1

US-09-894-749-2
; Sequence 2, Application US/09894749
; Patent No. US20020081683A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/894,749
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/244,314
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 235
; ORGANISM: Homo sapiens
; US-09-894-749-2

Query Match	100.0%	Score 1218	DB 9	Length 235
Best Local Similarity	100.0%	Pred. No. 6.7e-110		
Matches 235	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	METTLFFSQINMCESKEKTFKLIHSGKEETSKEAKIRAKEKRNRLSLLVQKPEFHED	60	
Db	1	METTLFFSQINMCESKEKTFKLIHSGKEETSKEAKIRAKEKRNRLSLLVQKPEFHED	60	
Qy	61	TRSRSGHLAKETRVSPPEEAVKNGESFDKLLSHRDGLEAPTRFLKTEFSEENIEFWIACE	120	
Db	61	TRSRSGHLAKETRVSPPEEAVKNGESFDKLLSHRDGLEAPTRFLKTEFSEENIEFWIACE	120	
Qy	121	DFKSKGPGQIHLKAKAIYEKFTQTDAPKEVNLDFHTKEVITNSITQPTLHSPDAQSRV	180	
Db	121	DFKSKGPGQIHLKAKAIYEKFTQTDAPKEVNLDFHTKEVITNSITQPTLHSPDAQSRV	180	
Qy	181	YQLEMEQSDYTRFLKSDIYLDLMEGRQPTNLRRRRSRSTFCNEFDQVSDVAIWL	235	

Db 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNFQDVQSDVAIWL 235
|||||
RESULT 2
US-10-258-371B-20
; Sequence 20, Application US/10258371B
; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Alison
; APPLICANT: MURRAY, David L.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
; TITLE OF INVENTION: RGS18, AND USES THEREOF
; FILE REFERENCE: A3656 US PCT
; CURRENT APPLICATION NUMBER: US/10/258,371B
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: GB001883.334
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/200,786
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-371B-20
Query Match 100.0%; Score 1218; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 6.7e-110;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 METTLLFSSQINNCESKKTFFKLHSGKETSKEAKIRAKEKRNRLSLVQKPEFHED 60
Db 1 METTLLFSSQINNCESKKTFFKLHSGKETSKEAKIRAKEKRNRLSLVQKPEFHED 60
Qy 61 TRSSRSGLAKETRVSPEAVKWSGSDKLLSHRDGLEAFTFLKTEFSEENIEFWACE 120
Db 61 TRSSRSGLAKETRVSPEAVKWSGSDKLLSHRDGLEAFTFLKTEFSEENIEFWACE 120
Qy 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQSRV 180
Db 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQSRV 180
Qy 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNFQDVQSDVAIWL 235
Db 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNFQDVQSDVAIWL 235
|||||
RESULT 3
US-09-867-550-848
; Sequence 848, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US96/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-848

Query Match 96.6%; Score 1176; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 7.7e-106;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 METTLLFSSQINNCESKKTFFKLHSGKETSKEAKIRAKEKRNRLSLVQKPEFHED 60
Db 1 METTLLFSSQINNCESKKTFFKLHSGKETSKEAKIRAKEKRNRLSLVQKPEFHED 60
Qy 61 TRSSRSGLAKETRVSPEAVKWSGSDKLLSHRDGLEAFTFLKTEFSEENIEFWACE 120
Db 61 TRSSRSGLAKETRVSPEAVKWSGSDKLLSHRDGLEAFTFLKTEFSEENIEFWACE 120
Qy 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQSRV 180
Db 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQSRV 180
Qy 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNFQDV 227
Db 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNFQDV 227
|||||
RESULT 4
US-09-894-749-4
; Sequence 4, Application US/09894749
; Patent No. US20020081683A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/894,749
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/244,314
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-894-749-4
Query Match 84.7%; Score 1032; DB 9; Length 235;
Best Local Similarity 83.8%; Pred. No. 7.7e-92;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
Qy 1 METTLLFSSQINNCESKKTFFKLHSGKETSKEAKIRAKEKRNRLSLVQKPEFHED 60
Db 1 MDMSLVFSSQINNCESKKTFFKLHSGKETSKEAKIRAKEKRNRLSLVQKPEFHED 60
Qy 61 TRSSRSGLAKETRVSPEAVKWSGSDKLLSHRDGLEAFTFLKTEFSEENIEFWACE 120
Db 61 TQASRSALLAKETRVSPEAVKWSGSDKLLSHRDGLEAFTFLKTEFSEENIEFWACE 120
Qy 121 DFKSKGPGQIHLKAKAIYEKFIQTDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQSRV 180
Db 121 DFKKCKEPPQIILKAKAIYEKFIQTDAPKEVNLDPHTKEVITNSITQPTLHSDFAAQSRV 180
Qy 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNFQDVSDVAIWL 235
Db 181 YQMEHDSYTRFLKSETYLHLEGRPQPTNLRSSRSFTCNFQDVSDVAIWL 235
|||||
RESULT 5
US-09-206-639-4
; Sequence 4, Application US/09206639
; Patent No. US20020034777A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Goli, Surya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,639
; FILING DATE: 07-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/748,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0157 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 292037
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-206-639-4

Query Match 34.7%; Score 422.5; DB 9; Length 211;
Best Local Similarity 42.8%; Pred. No. 1e-32;
Matches 89; Conservative 37; Mismatches 73; Indels 9; Gaps 3;
QY 6 LFFSQINMCESKEKTFKLIHSGKSEKAKIR---AKEKNRRLSLLVQKPEFHEDTR 62
DB 5 MFLAVQHDCRPMDKS-----AGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGPK 59
QY 63 SRSRSHLAKETRVSPPEAVKVGESFDKLLSHRDGLEAFTRFLKTEFSEENIEFWIACEDF 122
DB 60 TGKSKQQAIFKPSPEAQWLSEAFDELLASKYGLAAFRFLKSEFCEENIEFWIACEDF 119
QY 123 KKSQGPQIHLKAKAIYEKFIQTDPKENVLDHPTKEVITNSITQPTLHSDFAAQSRVYQ 182
DB 120 KTKSPQKLSSKARKIYTDPIEKEAPKEINIDFQTKLIAQNIQEAATSGCFTTAQKRVS 179
QY 183 LMEQDSYTRFLKSDIYLDLMGCRPQPT 210
DB 180 LMENNSYPRFLESEFYQDLCK-KPQITT 206

RESULT 7
US-10-408-765A-493
; Sequence 493, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 493
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-493

Query Match 34.7%; Score 422.5; DB 16; Length 211;
Best Local Similarity 42.8%; Pred. No. 1e-32;
Matches 89; Conservative 37; Mismatches 73; Indels 9; Gaps 3;
QY 6 LFFSQINMCESKEKTFKLIHSGKSEKAKIR---AKEKNRRLSLLVQKPEFHEDTR 62
DB 5 MFLAVQHDCRPMDKS-----AGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGPK 59
QY 63 SRSRSHLAKETRVSPPEAVKVGESFDKLLSHRDGLEAFTRFLKTEFSEENIEFWIACEDF 122
DB 60 TGKSKQQAIFKPSPEAQWLSEAFDELLASKYGLAAFRFLKSEFCEENIEFWIACEDF 119
QY 123 KKSQGPQIHLKAKAIYEKFIQTDPKENVLDHPTKEVITNSITQPTLHSDFAAQSRVYQ 182
DB 120 KTKSPQKLSSKARKIYTDPIEKEAPKEINIDFQTKLIAQNIQEAATSGCFTTAQKRVS 179

US-10-258-371B-24
; Sequence 24, Application US/10258371B
; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Alison
; APPLICANT: MURRAY, David L
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
; FILE REFERENCE: RGS18, AND USES THEREOF
; FILE REFERENCE: A3656 US PCT
; CURRENT APPLICATION NUMBER: US/10/258,371B
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: GB001833.334

Query Match 33.9%; Score 413; DB 12; Length 81;
Best Local Similarity 97.5%; Pred. NO. 2.3e-32;
Matches 78; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 110 BENISFWIACEDFKSKGPGQIHLKAKAIYEKFIQTDPAPKEVNLDFHTKEVITNSITQPT 169
DB 2 ENLFWIACEDFKSKGPGQIHLKAKAIYEKFIQTDPAPKEVNLDFHTKEVITNSITQPT 61
QY 170 LHSFDAQSRVYQLMEQDSY 189
DB 62 LHSFDAQSRVYQLMENDSY 81
RESULT 14
US-10-398-953-1
; Sequence 1, Application US/10398953
; Publication NO. US20030186304A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: NO. US20030186304A1el disease-associated gene and use thereof
; FILE REFERENCE: 2801 USCP
; CURRENT APPLICATION NUMBER: US/10/398,953
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: JP 2000-319912
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: JP 2000-350183
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Rat
US-10-398-953-1
Query Match 33.7%; Score 410.5; DB 14; Length 181;
Best Local Similarity 48.2%; Pred. NO. 1.2e-31;
Matches 80; Conservative 35; Mismatches 48; Indels 3; Gaps 1;
QY 40 RAKEKRNRLSLIVQKPEPHED---TRSRSGHLAKETRVSPPEAVKVGESFDKLLSHRDG 96
DB 15 RAKEIKIKLIGLLQKPDSDAVLVIPEYNEKPKPAKAKPSLEEVQLWQSLDKLLQSNYG 74
QY 97 LEAFTRFLKTEFSEENIEFWIACEDFKSKGPGQIHLKAKAIYEKFIQTDPAPKEVNLDFH 156
DB 75 PASPKSFLKSEFSEENIEFWIACEDFKSKGPGQIHLKAKAIYEKFIQTDPAPKEVNLDFH 134
QY 157 TKEVITNSITQPTLHSDFAAQSRVYQLMEQDSYTRFLKSDIYLDLM 202
DB 135 TKDITMKNLVEPSHPSFDLAQRIYALMEKOSLPRFVRSEFYKELI 180

RESULT 15
US-10-113-794A-1
; Sequence 1, Application US/10113794A
; Publication NO. US20030022202A1
; GENERAL INFORMATION:
; APPLICANT: Flanagan et al.
; TITLE OF INVENTION: B EPHRIN REGULATION OF G-PROTEIN COUPLED
; FILE REFERENCE: 2535/106
; CURRENT APPLICATION NUMBER: US/10/113,794A
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-113-794A-1
Query Match 33.6%; Score 409; DB 14; Length 930;
Best Local Similarity 45.3%; Pred. NO. 1.6e-30;

Matches 82; Conservative 37; Mismatches 60; Indels 2; Gaps 1;
QY 31 ETSKEAKTR--AKEKRNRLSLIVQKPEPHEDTRSRSGHLAKETRVSPPEAVKVGESFD 88
DB 748 DEASRRKSKNIAKDKMKNKLAIFRRRNESPGQAQPAKTDKTTKSPKPTSEALKWSELE 807
QY 89 KLLSHEDGLEAFTRFLKTEFSEENIEFWIACEDFKSKGPGQIHLKAKAIYEKFIQTDPAP 148
DB 808 KLLHXYGLLEVQAFRLTEFSEENIEFWIACEDFKSKGPGQIHLKAKAIYEKFIQTDPAP 867
QY 149 KEVNLDFTKEVITNSITQPTLHSDFAAQSRVYQLMEQDSYTRFLKSDIYLDLMGRFOR 208
DB 868 KEVNLDFTKEVITNSITQPTLHSDFAAQSRVYQLMEQDSYTRFLKSDIYLDLMGRFOR 927
QY 209 P 209
DB 928 P 928
Search completed: August 20, 2004, 17:06:39
Job time : 241 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2004, 16:14:26 ; Search time 25 Seconds
(without alignments)
904.200 Million cell updates/sec

Title: US-09-894-749-2

Perfect score: 1218

Sequence: 1 METLLPFSQINMCSEKKT.....SRSTFCNEFQDVQSDVAINL 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Pir1.*
- 2: Pir2.*
- 3: Pir3.*
- 4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	422.5	34.7	211	2	I53020
2	408.5	33.5	205	2	S78221
3	404	33.2	519	2	S78089
4	400.5	32.9	181	2	JC7228
5	346	28.4	196	2	S43436
6	315.5	25.9	181	2	T21035
7	313.5	25.7	251	2	S43526
8	313.5	25.7	254	2	G85711
9	313	25.7	169	2	T21034
10	312	25.6	244	2	T13580
11	282.5	23.2	173	2	S71812
12	278.5	22.9	533	2	T31002
13	243.5	20.0	544	2	JC5503
14	225	18.5	1387	2	JC5502
15	220	18.1	473	2	T19337
16	216	17.7	558	2	T21468
17	215.5	17.7	234	2	T26672
18	208	17.1	838	2	T08423
19	194.5	16.0	832	2	T08422
20	178.5	14.7	270	2	T22213
21	178.5	14.7	284	2	T15700
22	158.5	13.0	274	2	T22214
23	149	12.2	235	2	F89472
24	141	11.6	719	2	S60771
25	135	11.1	303	2	T29513
26	116	9.5	229	2	A89473
27	114	9.4	1010	2	T41077
28	113.5	9.3	209	2	S61665
29	102.5	8.4	688	1	JC1469

30	101.5	8.3	688	1	A39336	beta-adrenergic-re
31	98	8.0	1092	2	T12520	hypothetical prote
32	97	8.0	423	2	T15335	hypothetical prote
33	97	8.0	913	2	T31497	hypothetical prote
34	96.5	7.9	950	2	F86286	hypothetical prote
35	95.5	7.8	1246	2	S60954	probable membrane
36	95	7.8	1187	2	T18355	hypothetical prote
37	94	7.7	997	1	I54390	phosphoinositide-s
38	94	7.7	1319	2	A28313	glued protein - fr
39	93.5	7.7	1514	2	S70099	hypothetical prote
40	93	7.6	258	2	T03447	hypothetical prote
41	92.5	7.6	535	2	E37189	hypothetical prote
42	92.5	7.6	537	2	E96681	protein F1822.4 [i
43	91.5	7.5	393	2	H83747	two-component sens
44	91.5	7.5	480	2	S72668	oviduct-specific p
45	91.5	7.5	3418	1	G02334	breast cancer tumo

ALIGNMENTS

RESULT 1

I53020

G-0/G-1 switch regulatory protein 8 - human

N;Alternate names: helix-loop-helix phosphoprotein; regulator of G-protein signaling 2, ;

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C;Accession: I53020; I65984

R;Siderovski, D.P.; Heximer, S.P.; Forsdyke, D.R.

DNA Cell Biol. 13, 125-147, 1994

A;Title: A human gene encoding a putative basic helix-loop-helix phosphoprotein whose mR

A;Reference number: I53020; MUID:94235158; PMID:8179820

A;Accession: I53020

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-211 <RES>

A;Cross-references: GB:I13391; NID:9292036; PIDN:AAA20680.1; PID:9292037

A;Accession: I65984

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-211 <RE2>

A;Cross-references: GB:I13463; NID:9292054; PIDN:AAC37587.1; PID:9292055

C;Genetics:

A;Gene: GDB:RGS2; GOS8

A;Cross-references: GDB:355647; OMIM:600861

A;Map position: lq31-lq31

A;Introns: 37/2; 71/2; 92/1; 147/3

C;Superfamily: B-cell activation protein BL34

C;Keywords: phosphoprotein

Query Match 34.7%; Score 422.5; DB 2; Length 211;

Best Local Similarity 42.8%; Pred.No. 3.3e-25; Mismatches 37; Indels 9; Gaps 3;

Matches 89; Conservative 37; Mismatches 73; Indels 9; Gaps 3;

Qy 6 LPFSQINMCSEKKTFFKLHSGKSETSKEAKIR---AKERNRLSLVQPEFHEDTR 62

Db 5 MFLAVQHDRCRPMDKS-----AGSGHKSEBKREKMTLLKDWKTRLSYFLQNSSTPGKPK 59

Qy 63 SRSRHLAKETRVSPPEAVKWSPEFKLSHRDGLAEAFTRFLKTFPSENIWFACEDP 122

Db 60 TGKKSQQAIFKPSPEEAQWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACEDP 119

Qy 123 KKSQGPQQLHAKAIYKFIQTDAPEKNVLDPHTKEVITNSITQPTLHSDFAAQSRVYQ 182

Db 120 KKTSPQKLSKARKYTDYFIEKEAPEKNIDFQKTLIAQNIQEQATSGCFTTAQKRIVS 179

Qy 183 LMEQDSYTRFLKSDIYLDMEGRPQRPPT 210

Db 180 LMENNSYPRFLESEFYQDLCK-KPQITT 206

RESULT 2

S78221


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A/Accession: I56185
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-180; 'D', 182-196 >HID>
A/Cross-references: GB:S59049; PID:g299704; PID:ARB26289.1; PID:g299705
C/Genetics:
A/Gene: GDB:RGS1; IER1; IR20; IR20; BL34
A/Cross-references: GDB:439178; OMIM:600323
A/Map position: 1q31-1q31
C/Superfamily: B-cell activation protein BL34
C/Keywords: B-cell; phosphoprotein

Query Match      28.4%; Score 346; DB 2; Length 196;
Best Local Similarity 45.9%; Pred. No. 2.1e-19;
Matches 68; Conservative 29; Mismatches 45; Indels 6; Gaps 2;

QY 55 PEFHEDTRSSRSHLAKETRVSPPEAVKMGSEFDKLLSHRDGLAEAFTRFLKTEFSEENIE 114
Db 46 PHESEGMMKSSKSDV-----LSAAEVQWQSLEKLLANQTGVNFGSFLKSEFSEENIE 100
QY 115 FWIACEDFKSKSGPQQIHLKAKAIEYKFIOTDAPKEVNLDPHTKEVITNSITQPTLHSFD 174
Db 101 FWLACEDYKKTES-DLIFCKAEIYKAPVHSDAAQKINIDFTRESTAKKIKAPTPTCFD 159
QY 175 AAQSRVYQLMEQDSYTRFLKSDIYLDLM 202
Db 160 EAQKVIVTLMEKDSYPRFLKSHIYNLL 187

RESULT 6
T21035
hypothetical protein F16H9.1b - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C/Accession: T21035, T21272
R/Gardner, A.
submitted to the EMBL Data Library, July 1995
A/Reference number: Z19363
A/Accession: T21035
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-181 <W1L>
A/Cross-references: EMBL:Z50005; PIDN:CA854219.1; GSPDB:GN00028; CESP:F16H9.1b
A/Experimental source: Clone F16H9
R/Gardner, A.
submitted to the EMBL Data Library, November 1995
A/Reference number: Z19398
A/Accession: T21272
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-181 <W1L>
A/Cross-references: EMBL:Z67882; PIDN:CA854230.1; GSPDB:GN00028; CESP:F16H9.1b
A/Experimental source: clone F22E10
C/Genetics:
A/Gene: CESP:F16H9.1b
A/Map position: X
A/Introns: 28/2; 43/2; 54/1; 103/3
C/Superfamily: B-cell activation protein BL34

Query Match      25.9%; Score 315.5; DB 2; Length 181;
Best Local Similarity 33.2%; Pred. No. 4e-17;
Matches 67; Conservative 37; Mismatches 67; Indels 31; Gaps 2;

QY 1 METLLFPQINMCSEKTEKFFKLHSGSGKEETSKEAKIRAKEKRNLSLLVQKPEFHED 60
Db 1 MSCAISCFGIIVCVTNS-----PSGRPYVSGSVSVKKNQEN----- 40
QY 61 TRSSRSHLAKETRVSPPEAVKMGSEFDKLLSHRDGLAEAFTRFLKTEFSEENIEFWIACE 120
Db 41 -----DGPPTVEIVFGWSQFENLMKHRAGQKYFAEFLKGYSDENILFWQACE 89
QY 121 DFKKSGPQQIHLKAKAIEYKFIOTDAPKEVNLDPHTKEVITNSITQPTLHSFDAQSRV 180

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Db 299 EINNEGFLNKKOGRKONFFQKVR-----ROTFFEDAFATGVSSAGSSVI 345
Qy 66 SGHLAKETRIV-----SPEEAVKWSGSPDKLLSHRD 95
Db 346 SNTTGGVRIALKVIGPIRSLTSLYLRKMDLALSTSLYPSRDDVRQWEISFESLLNKF 405
Qy 96 GLEAFTRFLKTFESENIEFWIACEDFKK-GPQOIHAKAIYEKFIQTDAPEVNLD 154
Db 406 GCAUFRQLKKEFSDENDFLECEEFKQKDKGKSTTKQAEIYSFVFAHSPREVNLD 465
Qy 155 FHTKEVITNSI---TQPTLHSDFAAQSRVYQVLMEDQSYTRFLKSDIYDLDMEG-----RP 206
Db 466 SDTRAATKAAVEAGCKP--DIFALAAQSRVEQLMSKDSYRRRLDRDLFDLLLESYEITDKE 523
Qy 207 QRPYNLRRRS 216
Db 524 DKPSSSKDN 533

RESULT 13
JC5503
G-protein signaling regulator 14 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: JC5503
R:Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P.
Biochem. Biophys. Res. Commun. 233, 770-777, 1997
A:Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
A:Reference number: JC5502; MUID:97312490; PMID:9168931
A:Accession: JC5503
A:Molecule type: mRNA
A:Residues: 1-544 <SNO>
A:Cross-references: GB:U92279; NID:g2088555; PIDN:AAC53175.1; PID:g2088556
C:Comment: This protein functions as GTPase activating protein.
F:64-113/Domain: GH1 #status predicted <GH1>
F:117-152/Domain: GH2 #status predicted <GH2>
F:155-180/Domain: GH3 #status predicted <GH3>
F:514-534/Region: conserved #status predicted

Query Match 20.0%; Score 243.5; DB 2; Length 544;
Best Local Similarity 34.6%; Pred. No. 4.7e-11;
Matches 63; Conservative 30; Mismatches 6; Indels 27; Gaps 6;

Qy 59 EDTRSSRSGHLAKETRVP-----EEAVKWSGSPDKLLSHRDGLAEAFTRFLKTFESENIE 113
Db 35 EGRGSSLSIHSLPSPGSPFFS"DEQPVASWAQSPERLLQDPRGLAYFTEFLKKEFSAENV 94
Qy 114 EFWIACEDFKK--SKGPOQIHAKAIYEKFIQTDAPEVNLD---FHTKEVITNSITOP 168
Db 95 TFWQACERFQOIPASDTPKLAQEAHNIYHEFLSQALSPVNIHQAMLSEEV-----LAQP 150
Qy 169 TLHSDFAAQSRVYQVLMEDQSYTRFLKSDIYDLDM-----EGRFQR-----PTNLRRR 215
Db 151 RPDMPRAQLQIFNLKMFDSVAFVKSPLYQECLLAEAGREFLPNGSGSHLGSFDTARKK 210
Qy 216 SR 217
Db 211 PK 212

RESULT 14
JC5502
G-protein signaling regulator 12 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: JC5502
R:Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P.
Biochem. Biophys. Res. Commun. 233, 770-777, 1997
A:Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
A:Reference number: JC5502; MUID:97312490; PMID:9168931
A:Accession: JC5502
A:Molecule type: mRNA
```

```
A:Residues: 1-1387 <SNO>
A:Cross-references: GB:U92280; NID:g2088557; PIDN:AAC53176.1; PID:g2088558
C:Comment: This protein functions as GTPase activating protein. It interacts with ras-like
F:18-80/Domain: rhophilin-like #status predicted <RHO>
F:712-761/Domain: GH1 #status predicted <GH1>
F:765-800/Domain: GH2 #status predicted <GH2>
F:804-828/Domain: GH3 #status predicted <GH3>
F:1204-1220/Region: conserved #status predicted
F:1266-1295/Region: coiled heptad repeat (S-P-X-S-A)

Query Match 18.5%; Score 225; DB 2; Length 1387;
Best Local Similarity 29.7%; Pred. No. 3.8e-09;
Matches 68; Conservative 39; Mismatches 92; Indels 30; Gaps 6;

Qy 6 LFESQINCESKB-KTFPFKLHSGSKEETSKAKIRAKERKRLSLLLVQKPEFHED---- 60
Db 612 LFGPHRNVKTKEDKSKSLGRGVALAQISQTSARSFGRSRRLFTSLDLESATVS 671
Qy 61 -----TRSSRSGHLAKET-----RVSPPEAVKWSGSPDKLLSHRDGLAEAFTR 102
Db 672 DGBLTGADLKDCISNNLSNASLPSVQSCRLLRERRVASWAVSPERLLQDPVGVRYFSD 731
Qy 103 FLKTFESENIEFWIACEDFK--KSKGPOQIHAKAIYEKFIQTDAPEVNLDFTTKEV 160
Db 732 FLKKEFSEENILFWQACECFSHVPADHKELSYRAEIEFSKFLCSKATTFVNIDSOA-QL 790
Qy 161 ITNSITQPTLHSDFAAQSRVYQVLMEDQSYTRFLKSDIY---LDLMEGR 205
Db 791 ADDILNAPHDMEKEQQLQIFNLKMFDSYTRFLKSQLYQECVLAIEGR 839

RESULT 15
T19337
hypothetical protein C16C2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19337
R:Barlow, K.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19109
A:Accession: T19337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-473 <WIL>
A:Cross-references: EMBL:Z81036; PIDN:CAB02742.1; GSPDB:GN00019; CESP:C16C2.2
C:Genetics:
A:Gene: CESP:C16C2.2
A:Map position: 1
A:Introns: 7/3; 47/3; 75/3; 107/1; 133/2; 232/2; 270/2; 440/3; 469/2

Query Match 18.1%; Score 220; DB 2; Length 473;
Best Local Similarity 33.7%; Pred. No. 2.5e-09;
Matches 59; Conservative 29; Mismatches 67; Indels 20; Gaps 5;

Qy 57 FHEDTRSSRSGHLAKETRVPPEAVKWSGSPDKLLSHRDGLAEAFTRFLKTFESENIEFW 116
Db 263 FWNQPTDTSAAEPTKRVK-----RWGLSVQLVWDPIGRQVLETFLESEFSENIWF 317
Qy 117 IACEDFKKSGPOQIHAKAIYEKFIQTDAPEVNLDFTTKEVITNSITQPTLHSDFA 176
Db 318 IATQDLKAYFN-EQIYKAEIRIEEFIAQCAPAQAQVAVNDNRTLDQTLECIISK----AKDAS 372
Qy 177 QSR-----VYQLMEQDSYTRFLKSDIYDLDMEGRQRPQPNLRRRSFTCN 222
Db 373 QMRFAFYHSEEHVFTLMKDSYFRFVRSQIYKAVLTAQQHGTGK-RLGWRNFVN 426

Search completed: August 20, 2004, 16:47:48
Job time : 27 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2004, 12:32:00 ; Search time 14.5 Seconds
(without alignments)
843.896 Million cell updates/sec

Title: US-09-894-749-2

Perfect score: 1218

Sequence: 1 METLLFPQINMCSEKTEK.....SRFTCFQDVQSDVAIWL 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1218	100.0	235	1 RGS1_HUMAN	Qns28 homo sapien
2	1032	84.7	235	1 RGS1_MOUSE	Q9p944 mus musculus
3	422.5	34.7	211	1 RGS2_HUMAN	P41220 homo sapien
4	421.5	34.6	181	1 RGS5_HUMAN	O15539 homo sapien
5	418.5	34.4	211	1 RGS2_RAT	Q9jhx0 rattus norv
6	416.5	34.2	211	1 RGS2_MOUSE	O08849 mus musculus
7	410.5	33.7	181	1 RGS5_RAT	P49800 rattus norv
8	409	33.6	568	1 RGS3_MOUSE	Q9dc04 mus musculus
9	408.5	33.5	205	1 RGS4_HUMAN	P49798 homo sapien
10	405.5	33.3	205	1 RGS4_MOUSE	O08899 mus musculus
11	404.5	33.2	181	1 RGS5_MOUSE	O08850 mus musculus
12	404.5	33.2	205	1 RGS4_RAT	P49799 rattus norv
13	404	33.2	519	1 RGS3_HUMAN	P49796 homo sapien
14	402.5	33.0	180	1 RGS8_HUMAN	P57771 homo sapien
15	402.5	33.0	180	1 RGS8_RAT	P49804 rattus norv
16	380.5	31.2	196	1 RGS1_MOUSE	Q9j125 mus musculus
17	380	31.2	202	1 RGS6_HUMAN	O15492 homo sapien
18	378	31.0	202	1 RSGG_BOVIN	O46471 bos taurus
19	369	30.3	201	1 RSGG_MOUSE	P97428 mus musculus
20	365.5	30.1	199	1 RSGG_RAT	P56700 rattus norv
21	353	29.0	196	1 RGS1_HUMAN	Q08116 homo sapien
22	327.5	26.9	218	1 RSGK_CHICK	Q9pwal gallus gall
23	325	26.7	388	1 RSGK_HUMAN	O76081 homo sapien
24	324	26.6	239	1 RSGK_MOUSE	Q9gzbi mus musculus
25	318.5	26.1	374	1 RSGK_BOVIN	P99348 bos taurus
26	315	25.9	201	1 RSH_MOUSE	Q9gzbo mus musculus
27	313.5	25.7	201	1 RSL1_CAEEL	P44295 caenorhabdi
28	313	25.7	169	1 RSG2_CAEEL	P49808 caenorhabdi
29	311.5	25.6	216	1 RGSJ_RAT	O70521 rattus norv
30	309.5	25.4	210	1 RSGH_CHICK	Q9pwa0 gallus gall
31	309.5	25.4	216	1 RGSJ_MOUSE	Q9cx84 mus musculus
32	308.5	25.3	210	1 RSGH_HUMAN	Q9uc66 homo sapien
33	306	25.1	217	1 RGSJ_HUMAN	P49795 homo sapien

ALIGNMENTS

RESULT 1

ID	RGS1_HUMAN	STANDARD;	PRT;	235 AA.
AC	QNS28;	2001 (Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Regulator of G-protein signaling 18 (RGS18).			
GN	RGS18 OR RGS13			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhang W., Wan T., Yuan Z., He L., Cao X.;			
RT	"A novel regulator of G-protein signaling."			
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Platelet;			
RA	Gagnon A.W., Murray D.L., Leadley R.J. Jr.;			
RT	"cloning and characterization of a novel regulator of G-protein			
RT	signaling in human platelets."			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=11042171;			
RA	Park I.K., Klug C.A., Li K., Jerabek L., Li L., Nanamori M.,			
RA	Neubig R.R., Hood L., Weissman I.L., Clarke M.F.;			
RT	"Molecular cloning and characterization of a novel regulator of			
RT	G-protein signaling from mouse hematopoietic stem cells."			
RL	J. Biol. Chem. 276:915-923(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
EX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pearce C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,			
RA	Vallalon D.K., Mugny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Brakesley R.W., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalish D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			

Q9cqe5 mus musculus
O14921 homo sapien
O43665 homo sapien
Q92zh2 mus musculus
P49802 homo sapien
P49803 rattus norv
O46470 bos taurus
O75916 homo sapien
O54829 mus musculus
O54828 mus musculus
P49805 rattus norv
O46469 bos taurus

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Regulator of G-protein signaling 2 (RGS2) (GO/G1 switch regulatory
 DE protein 8)
 DE RGS2 OR G0S8.
 GN Homo sapiens (Human)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA MEDLINE=94233158; PubMed=8179920;
 RX Siderovski D.P., Heximer S.P., Forsdyke D.R.;
 RT "A human gene encoding a putative basic helix-loop-helix
 RT phosphoprotein whose mRNA increases rapidly in cycloheximide-treated
 RT blood mononuclear cells.";
 RL DNA Cell Biol. 13:125-147(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urinary bladder;
 RA MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Schaefer C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=95371353; PubMed=7643615;
 RA Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W.,
 RA Minden M.D., Siderovski D.P.;
 RT "Differential expression of a basic helix-loop-helix phosphoprotein
 RT gene, G0S8, in acute leukemia and localization to human chromosome
 RT 1q31.";
 RL Leukemia 9:1291-1298(1995).
 RN [6]
 RP PHOSPHORYLATION.
 RX MEDLINE=21101914; PubMed=11063746;
 RA Cunningham M.L., Waldo G.L., Hollinger S., Hepler J.R., Harden T.K.;
 RT "Protein kinase C phosphorylates RGS2 and modulates its capacity for
 RT negative regulation of G-protein signaling.";
 RL J. Biol. Chem. 276:5438-5444(2001).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACUTE MYELOGENOUS LEUKEMIA (AML)
 CC AND IN ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).

CC -!- PTM: Phosphorylated by protein kinase C.
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L13391; AAA20680.1; -;
 DR EMBL; L13463; AAC37587.1; -;
 DR EMBL; AF493926; AAM12640.1; -;
 DR EMBL; AL035407; CAB63512.1; -;
 DR EMBL; BC007049; AAH07049.1; -;
 DR PIR; I53020; I53020.
 DR HSP; P49799; IAGR.
 DR Genew; HGNC:9998; RGS2.
 DR MIM; 608661; -;
 DR GO; GO:0005516; F-actin modulin binding; TAS.
 DR GO; GO:0005096; F-GTPase activator activity; TAS.
 DR GO; GO:0008277; P-regulation of G-protein coupled receptor pr. .; TAS.
 DR InterPro; IPR000342; Regl_Gproteins.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN
 DR PRODOM; PD001580; Regl_Gproteins; 1.
 DR SMART; SM00315; RGS; 1.
 DR PROSITE; PS01332; RGS; 1.
 KW Signal transduction inhibitor; Cell cycle; Phosphorylation.
 FT DOMAIN 83 199
 SQ SEQUENCE 211 AA; 24382 MW; EFPB4AB47E9AD8F CRC64;
 Query Match 34.7%; Score 422.5; DB 1; Length 211;
 Best Local Similarity 42.8%; Pred. No. 3.4e-25;
 Matches 89; Conservative 37; Mismatches 73; Indels 9; Gaps 3;
 QY 6 LPSQINMCSEKTEKFKLHSGSKETSKEAKIR---AKEKENRLSLVQKPEFHEDTR 62
 DB 5 MFLAVQHDCEPMDXS-----AGSGHSEKREKMKETLLKDWKTRLSYFLQNSSTPGKPK 59
 QY 63 SRSRSHLAKETRVSPPEAVKNGESFKLLSHRDGLAFTFRFLKTEPSENIETFWIACEDF 122
 DB 60 TGKSKQQQAFIKPSPEEAQIWLSEAFDELLASKYGLAAFRFLKSEFCENIEFWLACEDF 119
 QY 123 KSKSGQQIHLKAKAIYERFIOTDAPKEVNDPHTKEVITNSTOPTLHSDFAAQSRVYQ 182
 DB 120 KTKSPQKSSKARKIYTFIKEAPKEINIDFQTKLIAQNIQEAATSCFTTAQKEVYS 179
 QY 183 LMEQDSYTRFLKSDIYLDLMEGRPQPT 210
 DB 180 LMENNSYPRFLESEFYQDLCK-KPQITT 206
 RESULT 4
 RGS5 HUMAN STANDARD; PRT; 181 AA.
 ID RGS5_HUMAN
 AC O15539;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Regulator of G-protein signaling 5 (RGS5).
 GN RGS5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chatterjee T.K., Fisher R.A.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kirsch T., Lippoldt A., Wellner M., Haller H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 95-161 FROM N.A.
 RX TISSUE=Brain;
 RC MEDLINE=96140645; PubMed=8548815;
 RA Koelle T.R., Horvitz H.R.;
 RT "EGF-10 regulates G protein signaling in the C. elegans nervous
 RL system and shares a conserved domain with many mammalian proteins.";
 CC [1]
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(1)-ALPHA AND G(O)-ALPHA,
 CC BUT NOT TO G(S)-ALPHA (BY SIMILARITY).
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC [2]
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 CC or send an email to license@isb-sib.ch).
 CC [3]
 CC EMBL; AF241259; RAE73424.1; --
 DR EMBL; U32435; AAC52372.1; --
 DR HSSP; P49799; IAGR.
 DR InterPro; IPR000342; RegI_Gprotein.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 DR ProDom; PD001580; RegI_Gprotein; 1.
 DR SMART; SM00315; RGS; 1.
 DR PROSITE; PS50132; RGS; 1.
 DR Signal transduction inhibitor.
 KW DOMAIN 64 180 RGS.
 FT SEQUENCE 181 AA; 21052 MW; 9C179CE008B2C03 CRC64;
 SQ
 Query Match 33.7%; Score 410.5; DB 1; Length 181;
 Best Local Similarity 48.2%; Pred. No. 2.2e-24;
 Matches 80; Conservative 35; Mismatches 48; Indels 3; Gaps 1;
 QY 40 RAKERNRLSLIVQPEPHED---TRSRSGHLAKETRVSPPEAVKKGESFDFKLLSHRDG 96
 DB 15 RAKEIKILGILLQKPSAVDLVPIYNEKPKAKAHKPSLEEVLRQSLDKLLQSNYG 74
 QY 97 LEAFTRFKTFSESENIWFACEDFKSKPQOIHAKAIYKFTQTDAPKEVNLDFH 156
 DB 75 FASPKFLKSEFSENLFEWACENYKIKSPKVAEKAKQIYEFIQTEAPKEVNDHF 134
 QY 157 TKEVITNSITPTLHSDFAAQSRVYQMLQEDSYTRFLKSDIYLDLM 202
 DB 135 TKDIITMKLVSPSPHSFLAQKRIYALMEKDSLPRFVSEFYKSLI 180
 RESULT 8
 RGS3 MOUSE
 ID_RGS3 MOUSE STANDARD; PRT; 568 AA.
 AC Q9DC04; Q9JL22; Q9JL23;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Regulator of G-protein signaling 3 (RGS3).
 GN RGS3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald W., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL [2]
 RN SEQUENCE FROM N.A. (ISOFORM LONG).
 RP STRAIN=FVB/N; TISSUE=Mammary gland;
 RC MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=20243574; PubMed=10779778;
 RA Reif K., Cyster J.G.;
 RT "RGS molecule expression in murine B lymphocytes and ability to
 RT down-regulate chemotaxis to lymphoid chemokines.";
 RL J. Immunol. 164:4720-4729(2000).
 CC -!- FUNCTION: Inhibits signal transduction by increasing the GTPase
 CC activity of G protein alpha subunits thereby driving them into
 CC their inactive GDP-bound form.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q9DC04-1; Sequences=Displayed;
 CC Name=Short;
 CC IsoId=Q9DC04-2; Sequences=VSP 005663, VSP 005664;
 CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
 CC similarity).
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC [4]
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DR PROSITE; PS0132; RGS; 1.
KW Signal transduction inhibitor; Lipoprotein; Palmitate;
FT Phosphorylation.
FT DOMAIN 62 178 RGS.
FT LIPID 2 2 S-palmitoyl cysteine (Probable).
FT LIPID 12 12 S-palmitoyl cysteine (Probable).
FT LIPID 95 95 S-palmitoyl cysteine.
FT LIPID 95 95 S-palmitoyl cysteine.
SQ SEQUENCE 205 AA; 23255 MW; 713FLF7496A698B CRC64;
Query Match 33.5%; Score 408.5; DB 1; Length 205;
Best Local Similarity 49.1%; Pred. No. 3.7e-24;
Matches 82; Conservative 28; Mismatches 48; Indels 9; Gaps 2;
QY 41 AKENRLLSVLQKPEFHEDTRSSRSHLAK-----TRVSPAAVKGESFDKLLSHRD 95
DB 16 AKDMKHLRGLFLQK-----SDCEHNSHNKKDKVVCORVSQEEVKWASLENLISHEC 71
QY 96 GLEAFTRFKTEFSENIETWIAEDFKSKGPOQIHLKAKAIYEKFIQTDAPKEVNLDF 155
DB 72 GLAARFALKEYSSENIETWIAEDFKSKGPOQIHLKAKAIYEKFIQTDAPKEVNLDF 131
QY 156 HTKEVITNSITQPTLHSDAQRVQLMEQDSYTRFLKSDIYLDLM 202
DB 132 CTRETSRNMLEPTTCFDEAQQKIFNLMEKDSYRFLKSRFYLDLV 178
RESULT 10
RGS4 MOUSE STANDARD; PRT; 205 AA.
AC O08659; Q99L30;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Regulator of G-protein signaling 4 (RGS4).
GN RGS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS76/6; TISSUE=Substantia nigra;
RX MEDLINE=98086343; PubMed=9425263;
RA Nomoto S., Adachi K., Yang L.X., Hirata Y., Muraguchi S., Kiuchi K.;
RT "Distribution of RGS4 mRNA in mouse brain shown by in situ
hybridization."
RL Biochem. Biophys. Res. Commun. 241:281-287(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO

CC THEIR INACTIVE GDP-BOUND FORM. ACTIVITY ON G(2)-ALPHA IS INHIBITED
BY PHOSPHORYLATION OF THE G-PROTEIN. ACTIVITY ON G(2)-ALPHA AND
G(1)-ALPHA-1 IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN (BY
SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN, MODERATELY
LOW LEVELS IN HEART, AND VERY LOW LEVELS IN LUNG, LIVER, AND
SKELETAL MUSCLE.
CC -!- PTM: Either Cys-2 or Cys-12 or both are palmitoylated (By
similarity).
CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
similarity).
CC -!- SIMILARITY: Contains 1 RGS domain.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; AB004315; BAA20400.1; --
CC ENBL; BC003882; AAB03882.1; --
CC HSSP; P49799; IAGR.
CC MGD; MGI:108409; Rgs4.
CC InterPro; IPR000342; Regl_Gprotein.
CC Pfam; PF00615; RGS; 1.
CC PRINTS; PR01301; RGS-PROTEIN.
CC ProDom; PD001580; Regl_Gprotein; 1.
CC SMART; SM00315; RGS; 1.
CC PROSITE; PS0132; RGS; 1.
CC Signal transduction inhibitor; Lipoprotein; Palmitate;
KW Phosphorylation.
FT DOMAIN 62 178 RGS.
FT LIPID 2 2 S-palmitoyl cysteine (By similarity).
FT LIPID 12 12 S-palmitoyl cysteine (By similarity).
FT LIPID 95 95 S-palmitoyl cysteine (By similarity).
FT CONFLICT 162 162 R > K (IN REF. 2).
FT SEQUENCE 205 AA; 23288 MW; 5D79581711A1P67C CRC64;
Query Match 33.3%; Score 405.5; DB 1; Length 205;
Best Local Similarity 50.0%; Pred. No. 6.2e-24;
Matches 81; Conservative 28; Mismatches 52; Indels 1; Gaps 1;
QY 41 AKENRLLSVLQKPEFHEDTRSSRSHLAKETRVSPAAVKGESFDKLLSHRDGLEA 99
DB 16 AKDMKHLRGLFLQKSDCEHNSHNKKDKVVCORVSQEEVKWASLENLISHCGLEA 75
QY 100 FTRFLKTEFSENIETWIAEDFKSKGPOQIHLKAKAIYEKFIQTDAPKEVNLDFHTKE 159
DB 76 FRAFLAKSEYSENIETWIAEDFKSKGPOQIHLKAKAIYEKFIQTDAPKEVNLDFHTKE 135
QY 160 VTNSTQPTLHSDAQRVQLMEQDSYTRFLKSDIYLDL 201
DB 136 ETSRNMLOPTTCFDEAQQKIFNLMEKDSYRFLKSRFYLDL 177
RESULT 11
RGS5 MOUSE STANDARD; PRT; 181 AA.
ID RGS5_MOUSE
AC O08650; Q9D022;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Regulator of G-protein signaling 5 (RGS5).
GN RGS5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236828; PubMed=9079700;
RX MEDLINE=97236828; PubMed=9079700;

Chen C., Zheng B., Han J., Lin S.C.;
 "Characterization of a novel mammalian RGS protein that binds to
 Galpha proteins and inhibits pheromone signaling in yeast.",
 J. Biol. Chem. 272:9679-9685(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kaikawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fieischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszah-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(O)-ALPHA,
 CC BUT NOT TO G(S)-ALPHA.
 CC -!- TISSUE SPECIFICITY: Expressed in heart and muscle.
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC
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 CC
 CC EMBL; U67188; AAB50618.1; -
 CC EMBL; AK004165; BAB23201.1; -
 CC EMBL; BC037683; AAB37683.1; -
 CC HSPB; P49799; IAGP
 CC MGD; MGI:1038434; Rgs5.
 CC InterPro; IPR000342; Regl_Gproteins.

Pfam: PF00615; RGS; 1.
 DR PRINTS; PRO1301; RGS-PROTEIN.
 DR ProDom; PD001580; Regl_Gproteins; 1.
 DR SMART; SMO0315; RGS; 1.
 DR PROSITE; PS0132; RGS; 1.
 KW Signal transduction inhibitor.
 FT DOMAIN 64 180 RGS.
 FT CONFLICT 49 50 KA -> NG (IN REF. 1).
 FT CONFLICT 77 77 S -> T (IN REF. 1).
 SQ SEQUENCE 181 AA; 21085 MW; B4B561CFE3DA9630 CRC64;
 Query Match 33.2%; Score 404.5; DB 1; Length 181;
 Best Local Similarity 47.3%; Pred. No. 6.4e-24;
 Matches 79; Conservative 37; Mismatches 48; Indels 3; Gaps 1;
 QY 40 RAKEKRNRLSLVQKPEFHED---TRSSSSGHLAKETRVSPBAVXWGSFDKLLSHRDG 96
 DB 15 RAKEIKIKGILLQKPSADVILVPTNEKPEKPAKAKPSLEVLQWRSCLKLQNSYG 74
 QY 97 LEAFTPLKTEFSEENIEFWIACEDFKGKGPQOHLKAKAIYEKFIQTDAPEVNLDFH 156
 DB 75 FASFKSLKSESEENLEFWACENYKKIKSPIKMAEKAKQIYEETQTEAPEKVNIDHF 134
 QY 157 TKEVINTSTQPTLHSHFDAAQSRVQVLMQEDSVTRPLKSDIYLDLME 203
 DB 135 TKDITMKNLVEPSRSPSFDLAQKRIYALMEKDSLPFRVSRSEFYKELIK 181
 RESULT 12
 RGS4_RAT STANDARD; PRT; 205 AA.
 AC P49799;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Regulator of G-protein signaling 4 (RGS4) (RGP4).
 GN RGS4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96178495; PubMed=8602223;
 RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
 RT "Inhibition of G-protein-mediated MAP kinase activation by a new
 RT mammalian gene family.";
 RL Nature 379:742-746(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Zhou M.-Y., Gomez-Sanchez C.E., Gomez-Sanchez E.P.;
 RT "The complete cDNA sequence analysis of the rat RGS4.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 93-159 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96140645; PubMed=8548815;
 RA Koelle M.R., Horvitz H.R.;
 RT "EGF-10 regulates G protein signaling in the C. elegans nervous
 RT system and shares a conserved domain with many mammalian proteins.";
 RL Cell 84:115-125(1996).
 RN [4]
 RP PHOSPHORYLATION.
 RX MEDLINE=20167219; PubMed=10702309;
 RA Pedram A., Razandi M., Kehrl J., Levin E.R.;
 RT "Natriuretic peptides inhibit G protein activation. Mediation through
 RT cross-talk between cyclic GMP-dependent protein kinase and regulators
 RT of G protein-signaling proteins.";
 RL J. Biol. Chem. 275:7365-7372(2000).
 RN [5]
 RP INHIBITION.
 RX MEDLINE=98016286; PubMed=9353196;

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QY      1  AKEXRNLISLVVKPFHFEDTSS-SRSCHLAKETRVSPPEAVKGGSGFDKLISHRDGLEA 99
DB      2  AKDWHRLGELLQKSCSCESSHSHSKDKVTCQRVSQEVEYKKWAEUSLENIINECGGLAA 75
QY      3  00 FTREKLTFFEESEENIEFWIACEDPKFKSGSQOHLHAKAIYSKFQTQDAPKEVNLDFTKE 159
DB      4  76 PKAFPLKSEYEENIDFWISCSEYKKIKSPKSLPRAKKIYNFISVQATKEVNLDSTCTRE 135
QY      5  160 VITNSITOPTILHSFDAQRSVQLMEQDSYTTRFLKSDIYDL 201
DB      6  136 ETSRNMLEPTITCFDEAQKIFNLMKESYRRFLKSRYLDL 177
QY      7  RESULT 13
DB      8  RGS3 HUMAN
QY      9  ID RGS3_HUMAN STANDARD; PRT; 519 AA.
DB     10  AC P49796; Q8TD59; Q8TD68;
QY     11  01-OCT-1996 (Rel. 34, Created)
DB     12  DT 01-OCT-1996 (Rel. 34, Last sequence update)
QY     13  DE 15-MAR-2004 (Rel. 43, Last annotation update)
DB     14  DE Regulator of G-protein signaling 3 (RGS3) (RGP3).
QY     15  OS Homo sapiens (Human).
DB     16  OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
QY     17  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DB     18  NCBI_TaxID=9606;
QY     19  [1]_
DB     20  RN SEQUENCE FROM N.A. (ISOFORM 1).
QY     21  RP MEDLINE=96178495; PubMed=8602223;
DB     22  RX Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
QY     23  RT "Inhibition of G-protein-mediated MAP kinase activation by a new
DB     24  RL mammalian gene family.";
QY     25  RL Nature 379:742-746(1996).
DB     26  RN [2]
QY     27  RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
DB     28  RC TISSUE=Brain;
QY     29  RA Publ H.L. III, Ikeda S.R., Aronstam R.S.;
DB     30  RA "cDNA clones of human proteins involved in signal transduction
QY     31  RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
DB     32  RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
QY     33  [3]
DB     34  RN SEQUENCE FROM N.A.
QY     35  RA Skuce C.;
DB     36  RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
QY     37  CC -! FUNCTION: Inhibits signal transduction by increasing the GRPase
DB     38  CC activity of G protein alpha subunits thereby driving them into
QY     39  CC their inactive GDP-bound form.
DB     40  CC -! ALTERNATIVE PRODUCTS:
QY     41  CC Event=Alternative splicing; Named isoforms=2;
DB     42  CC Name=1;
QY     43  CC IsoId=P49796-1; Sequence=Displayed;
DB     44  CC Name=2; Synonyms=RGS3T;
QY     45  CC IsoId=P49796-2; Sequence=VSP_005662;
DB     46  CC -! PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
QY     47  CC similarity).
DB     48  CC -! SIMILARITY: Contains 1 RGS domain.
QY     49  CC This SWISS-PROT entry is copyright. It is produced through a collaboration
DB     50  CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
QY     51  CC the European Bioinformatics Institute. There are no restrictions on its
DB     52  CC use by non-profit institutions as long as its content is in no way
QY     53  CC modified and this statement is not removed. Usage by and for commercial
DB     54  CC entities requires a license agreement (See http://www.isb-sib.ch/announcement
QY     55  CC or send an email to license@isb-sib.ch).
DB     56  CC -----
QY     57  CC ENBL; U27655; AAC50394.1; --
DB     58  CC ENBL; AF493927; AAM12641.1; --
QY     59  CC ENBL; AF493941; AAM12655.1; --
DB     60  CC ENBL; AL162727; CAC78977.1; --
QY     61  CC PIR; S78089; S78089.
DB     62  CC HSP; P49799; IAGR.
QY     63  CC Genew; HGNC:9999; RGS3.
DB     64  CC DR DR

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Query Match	33.2%;	Score 404.5;	DB 1;	Length 205;
Best Local Similarity	49.4%;	Pred. No. 7.4e-24;		
Matches	80;	Conservative	30;	Mismatches 51;
				Indels 1;
				Gaps 1;

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DR MIM; 602189;
DR GO; GO:0005829; C.cytosol; TAS
DR GO; GO:0005096; P.GTPase activator activity; TAS
DR GO; GO:0000188; P.inactivation of MAPK; TAS
DR GO; GO:0000827; P.inactivation of G-protein coupled receptor pr. .; TAS
DR InterPro; IPR000342; Regl_Gprotein.
DR Pfam; PF00615; RGS; 1
DR PRINTS; PR01301; RGS; 1
DR ProDom; PD001580; Regl_Gprotein; 1
DR SMART; SM00313; RGS; 1
DR PROSITE; PS50132; RGS; 1
KW Signal transduction inhibitor; Alternative splicing; Phosphorylation.
FT DOMAIN 394 510
FT DARSPLIC 1 313
FT FTID=Vsp 005662.
FT CONFLICT 305 305
FT SEQUENCE 519 AA; 56601 MW; FICFEP27D4673AO CRC64;
SQ
Query Match 33.2%; Score 404; DB 1; Length 519;
Best Local Similarity 44.2%; Pred. No. 2.5e-23;
Matches 80; Conservative 39; Mismatches 60; Indels 2; Gaps 1;
QY 31 EETSEAKIR--AKEKNRLSLVQKPEFHEDTRSSRSHLAKETRVSPPEAVKMGESFD 88
DB 337 DEAKRKRSKLNADKMKNGLIGFRRNESGAPGAKADKMKKFKPTSEALKMGESLE 396
QY 89 KLLSHRDGLAFTPLKTEFSEENIEFWIACEDFKKSGKQOIHAKAKAIYEKFIQTDPAP 148
DB 397 KLLVHKYGLAVFOAFLRTEFSEENLEFWLACEDFKKYSQSKASKAKKFAEVIATQAC 456
QY 149 KEVNLDFHTKEVINISITOPTLHFDAAQSRVQIMEDQSVTRFLKSDIYLDLMGEPQR 208
DB 457 KEVNLDSYTRHTKDNLSQSVTRGCFDLAQKIFGLMEKDSYFRLSRDLVLDLINQKMS 516
QY 209 P 209
DB 517 P 517
RESULT 14
RGS8 HUMAN STANDARD; PRT; 180 AA.
AC P5771,
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Regulator of G-protein signaling 8 (RGS8).
GN RGS8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=21218927; PubMed=11318611;
RA Sood R., Bonner T.I., Malakowska I., Stephan D.A., Robbins C.M.,
RA Connors T.D., Morgenbesser S.D., Su K., Faruque M.U., Pinkett H.,
RA Graham C., Baxevanis A.D., Klinger K.W., Landes G.M., Trent J.M.,
RA Carpton J.D.;
RT "Cloning and characterization of 13 novel transcripts and the human
RT RGS8 gene from the 1q25 region encompassing the hereditary prostate
RT cancer (HPC1) locus."
RL Genomics 73:211-222(2001).
[2]
SEQUENCE FROM N.A.
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. PREFERENTIALLY BINDS TO G(12)-ALPHA
CC AND G(11)-ALPHA-3 (BY SIMILARITY).
-!- SIMILARITY: Contains 1 RGS domain.
-----
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or send an email to license@isb-sib.ch).
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EMBL; AF297015; AAC45337.1; -
DR EMBL; AF300649; AAC18443.1; -
DR HSP; P49799; IAGR.
DR Genew; HGNC:16810; RGS8.
DR MIM; 607189;
DR InterPro; IPR000342; Regl_Gprotein.
DR Pfam; PF00615; RGS; 1
DR PRINTS; PR01301; RGS; 1
DR ProDom; PD001580; Regl_Gprotein; 1
DR SMART; SM00315; RGS; 1
DR PROSITE; PS50132; RGS; 1
KW Signal transduction inhibitor.
FT DOMAIN 56 171
FT CONFLICT 1 9
FT SEQUENCE 180 AA; 20917 MW; 198965B4C27F64C9 CRC64;
SQ
Query Match 33.0%; Score 402.5; DB 1; Length 180;
Best Local Similarity 46.5%; Pred. No. 9e-24;
Matches 80; Conservative 32; Mismatches 55; Indels 5; Gaps 2;
QY 40 RAKEKENRLSLVQKPEFHEDTRSSRSHLAKETRVSPPEAVKMGESFKLLSHRDG 96
DB 9 RNKGMRTRGLCLSHKSDSCSDFTAILDPKPNALK--RLSTBEATRWADSFVLLSHKYG 66
QY 97 LEAFTPLKTEFSEENIEFWIACEDFKKSGKQOIHAKAKAIYEKFIQTDPKAVNLDPH 156
DB 67 VAAFRALKTEFSEENLEFWLACEEFKTRSTAKLVSKAHRIFEEVDVQAPREVNIDFQ 126
QY 157 TKEVITNSITOPTLHFDAAQSRVQIMEDQSVTRFLKSDIYLDLMGEPQR 208
DB 127 TREATKLNQEPFLCFCDAQKQVHSLMEKDSYFRLSRDLVLDLINQKMS 178
RESULT 15
RGS8 RAT STANDARD; PRT; 180 AA.
AC P49804,
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of G-protein signaling 8 (RGS8).
GN RGS8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND FUNCTION.
RN RGS8=Hippocampus;
RX MEDLINE=96054153; PubMed=9394004;
RA Saich O., Kubo Y., Miyatani Y., Asano T., Nakata H.;
RT RGS8 accelerates G-protein-mediated modulation of K+ currents.";
RL Nature 390:525-528(1997).
[2]
SEQUENCE OF 87-153 FROM N.A.
RN RGS8=Brain;
RX MEDLINE=96140645; PubMed=8548815;
RA Koelle M.R., Horvitz H.R.;
RT "EGF-10 regulates G protein signaling in the C. elegans nervous
RT system and shares a conserved domain with many mammalian proteins.";
RL Cell 84:115-125(1996).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE

```

CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. PREFERENTIALLY BINDS TO G(O)-ALPHA
CC AND G(I)-ALPHA-3.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN. VERY
CC LITTLE EXPRESSION DETECTED IN OTHER TISSUES.
CC -!- DEVELOPMENTAL STAGE: DETECTED IN 13-DAY OLD EMBYOS. EXPRESSION
CC INCREASES GRADUALLY IN LATER EMBRYOS AND MARKEDLY IN NEONATES TO
CC ADULTS.
CC -!- SIMILARITY: Contains 1 RGS domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB006013; BAA23680.1; -.
DR EMBL; U32432; AAC52369.1; -.
DR HSSP; P49799; 1AGR.
DR InterPro; IPR000342; Regl_Gproteins.
DR Pfam; PF00615; RGS; 1
DR PRINTS; PRO1301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS01132; RGS; 1.
DR Signal transduction inhibitor.
FT DOMAIN 56 171 RGS.
SQ SEQUENCE 180 AA; 20949 MW; 00FC35E4C278E857 CRC64;

Query Match 33.0%; Score 402.5; DB 1; Length 180;
Best Local Similarity 46.5%; Pred. No. 9e-24;
Matches 80; Conservative 32; Mismatches 55; Indels 5; Gaps 2;

QY 40 RAKEKRNLSLLVQPEPHEDTRS--SRSGHLAKETRVSPPEAVKMGESGDKLLSHRDG*96
DB 9 RNKGKRTLGLCLSHKSDSCSDFTAILDPKPNRAK--RLSTEEATRWADSEFDVLLSHKYG 66
QY 97 LEAFTRFLKTEFSEENIEFWIACDFKSKGQQIHLKAKAIYKFKIOTDAPKEVNLDFH 156
DB 67 VAAFPRAFLKTEFSEENLSEFWLACEFKTKRSTAKLVTKAHRIFFEEFVDVQAPREVNIQ 126
QY 157 TKEVITNSITQPTLHSDFAAQSRVYQVLMQDSYTRFLKSDIYLDIMEGRPOR 208
DB 127 TREATKKNQEPSELTCTCFDQAGKQVHSLMEKOSYFRFLKRWMLDLLLSQSQR 178

Search completed: August 20, 2004, 16:41:29
Job time : 25.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2004, 15:52:01 ; Search time 74.5 Seconds
(without alignments)
995.259 Million cell updates/sec

Title: US-09-894-749-2

Perfect score: 1218

Sequence: 1 METLLFFSQINMCSEKTE.....SRSTCFNQDVQSDVAIWL 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	423.5	34.8	213	13	Q7ZZS4
2	423.5	34.8	225	13	Q7ZZS5
3	416	34.2	283	13	Q7SYI2
4	416	34.2	408	13	Q7SYI1
5	416	34.2	441	13	Q7SYI0
6	416	34.2	799	13	Q7SYH9
7	413	33.9	182	13	Q7TD23
8	410.5	33.7	208	13	Q7SCC6
9	409	33.6	930	11	Q925G9
10	408.5	33.5	181	6	Q86422
11	405.5	33.3	180	11	Q8BX11
12	404	33.2	917	4	Q8NFX4
13	404	33.2	917	4	Q8WXA0
14	404	33.2	917	4	Q8IU01
15	404	33.2	1093	4	Q8NFN5
16	403	33.1	967	11	Q920Q9

17	402	33.0	132	4	Q8WVE9	Q8wve9 homo sapien
18	401.5	33.0	136	6	Q9SK68	Q9SK68 macaca fasc
19	401	32.9	132	4	Q8WV02	Q8wv02 homo sapien
20	400	32.8	284	4	Q96NV5	Q96nv5 homo sapien
21	400	32.8	319	4	Q8NFN6	Q8nfn6 homo sapien
22	399.5	32.8	164	6	Q8HXV9	Q8hvx9 ovis aries
23	391	32.1	168	13	Q7SVI3	Q7svi3 gallus gall
24	369	30.3	235	11	Q8VVI6	Q8vvi6 mus musculu
25	366.5	30.1	204	13	Q919D9	Q919d9 xenopus lae
26	365.5	30.0	201	11	Q7TNU9	Q7tnu9 mus musculu
27	328	26.9	271	5	Q9V888	Q9v888 drosophila
28	328	26.9	274	5	Q8T017	Q8t017 drosophila
29	324	26.6	208	11	Q8CSJ7	Q8csj7 mus musculu
30	323	26.5	220	13	Q7TQO6	Q7tqo6 xenopus lae
31	321	26.4	220	13	Q8QHK0	Q8qhko xenopus lae
32	317	26.0	210	11	Q8CSF3	Q8csf3 mus musculu
33	316	25.9	230	11	Q8BR34	Q8br34 mus musculu
34	315.5	25.9	181	5	Q9TVK0	Q9tvko caenorhabdi
35	312.5	25.7	199	13	Q8AYF2	Q8ayf2 gallus gall
36	312	25.6	244	5	Q96842	Q96842 drosophila
37	309.5	25.4	194	11	Q8BFU4	Q8bfu4 mus musculu
38	307	25.2	150	4	Q8TD61	Q8td61 homo sapien
39	306.5	25.2	194	11	Q8CGT5	Q8cgt5 mus musculu
40	286.5	23.5	181	4	Q96GN0	Q96gn0 homo sapien
41	286	23.5	158	11	Q8K443	Q8k443 mus musculu
42	284.5	23.4	475	4	Q7Z4K3	Q7z4k3 homo sapien
43	284.5	23.4	477	4	Q7Z4K4	Q7z4k4 homo sapien
44	284.5	23.4	480	4	Q7Z4K5	Q7z4k5 homo sapien
45	281.5	23.1	424	5	Q95Q48	Q95q48 caenorhabdi

ALIGNMENTS

RESULT 1

Q7ZZS4 PRELIMINARY; PRT; 213 AA.

AC Q7ZZS4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Regulator of G-protein signaling protein 2.
GN RGS2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tosetti P., Parente V., Taglietti V., Dunlap K., Toselli M.;
RT "Concentration-dependent effects of chick RGS2L on neuronal L-type Ca channel modulation by bradykinin."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF502149; AAP30802.1;
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPR000342; Regl_Gpotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gpotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS00132; RGS; 1.
SQ SEQUENCE 213 AA; 24786 MW; B0CAD39ACC496D1E CRC64;

Query Match 34.8%; Score 423.5; DB 13; Length 213;
Best Local Similarity 46.9%; Pred. No. 1.2e-26;
Matches 84; Conservative 34; Mismatches 58; Indels 3; Gaps 1;

Qy 31 ETSSEAKIR---AKEKNRSLLVQKEFFHEDTSSRSCHLAKETRVSPPEAVWGSEF 87

Db 27 EADKGRMKRTIIDWKKKLSFYIUNSRSSKSKTKAGKHHTYFRPSPPEARLWSEAF 86

Qy 88 DKLLSHRDGLEAFTRFLKTFESENIEFWIACEDFKGKGPQOIHLKAKAIYEKTIQDTA 147

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120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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RT "RGS3 mediates a calcium-dependent termination of G protein signaling
RT in sensory neurons."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7337-7342 (2003).
DR EMBL; AY124774; AAM94020.1; -.
SQ SEQUENCE 283 AA; 32070 MW; 5C9871357F00A195 CRC64;

Query Match 34.2%; Score 416; DB 13; Length 283;
Best Local Similarity 47.7%; Pred. No. 6.6e-26;
Matches 83; Conservative 36; Mismatches 53; Indels 2; Gaps 1;

QY 31 ETSKEAKIR--AKEKNRLSLVQKPEFHEDTRSSRSHLAKETRVSPPEAVKWSGFD 88
DB 101 ETSRKRSLAKDMKNLGIFFRRNESPGANPSSKLDKVLKSLKPAPEALKWGESLE 160
QY 89 KLLSHRDGLEAFTFLKTEFSEENIEFWIACEDFKSKGPOQIHLKAKAIYEKTIQTDA 148
DB 161 KLLHKYGLAFAFRAFLRTEFSEENIEFWIACEDFKSKGPOQIHLKAKAIYEKTIQTDA 220
QY 149 KEVNLDFHTKEVITNSITQPTLHSDFAAQSRVQLMEQDSYTRFLKSDIYLDLM 202
DB 221 KEVNLDFHTKEVITNSITQPTLHSDFAAQSRVQLMEQDSYTRFLKSDIYLDLM 274

RESULT 4
Q7SVI1 PRELIMINARY; PRT; 408 AA.
AC Q7SVI1;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Regulator of G protein signaling 3 RGS3s isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DRG neuron; PubMed=12711384;
RX MEDLINE=22684492; Jacob M.H., Dunlap K.;
RA Tosetti P., Pathak N., Jacob M.H., Dunlap K.;
RT "RGS3 mediates a calcium-dependent termination of G protein signaling
RT in sensory neurons."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7337-7342 (2003).
DR EMBL; AY124775; AAM94021.1; -.
SQ SEQUENCE 408 AA; 45438 MW; 75B50794F22E74B5 CRC64;

Query Match 34.2%; Score 416; DB 13; Length 408;
Best Local Similarity 47.7%; Pred. No. 1e-25;
Matches 83; Conservative 36; Mismatches 53; Indels 2; Gaps 1;

QY 31 ETSKEAKIR--AKEKNRLSLVQKPEFHEDTRSSRSHLAKETRVSPPEAVKWSGFD 88
DB 226 ETSRKRSLAKDMKNLGIFFRRNESPGANPSSKLDKVLKSLKPAPEALKWGESLE 285
QY 89 KLLSHRDGLEAFTFLKTEFSEENIEFWIACEDFKSKGPOQIHLKAKAIYEKTIQTDA 148
DB 286 KLLHKYGLAFAFRAFLRTEFSEENIEFWIACEDFKSKGPOQIHLKAKAIYEKTIQTDA 345
QY 149 KEVNLDFHTKEVITNSITQPTLHSDFAAQSRVQLMEQDSYTRFLKSDIYLDLM 202
DB 346 KEVNLDFHTKEVITNSITQPTLHSDFAAQSRVQLMEQDSYTRFLKSDIYLDLM 399

RESULT 5
Q7SVI2 PRELIMINARY; PRT; 441 AA.
AC Q7SVI2;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Regulator of G protein signaling 3 (Fragment).
OS Gallus gallus (Chicken).

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RESULT 7					
Q7T2D3 PRELIMINARY; PRT; 182 AA.					
ID	Q7T2D3				
AC	Q7T2D3;				
DT	01-OCT-2003 (TrEMBLrel. 25, Created)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Brachydanio rerio (Zebrafish) (Danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio.				
OX	NCBI_taxid=7995;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISUE=Kidney;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Locuelli N.A., Peters G.J., Abramsen R.D., Mullany S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulys S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley A.C., Trichwood J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Groomwood J., Schmutz J., Myers R.M., Butterfield V.S.,				
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RL	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RP	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISUE=Kidney;				
RA	Strausberg R.;				
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC054594; RAH54594.1; -.				
KW	Hypothetical protein.				
SQ	SEQUENCE 182 AA; 21053 MW; 4D502817AA8CE4FF CRC64;				
Query Match 33.9%; Score 413; DB 13; Length 182;					
Best Local Similarity 49.7%; Pred. No. 6.8e-26;					
Matches 85; Conservative 29; Mismatches 47; Indels 10; Gaps 2;					
QY	40 RAKEKRNRLSLVQKPEP-----HEPTRSRSGHLAKETRVSPBEAVKWGESFDKLKS 92				
Db	15 RAKEIKTKGLTLQKPENSIDLIIYQEKPEKKPKLOKAT---PFEAAQWRSLDKVLS 71				
QY	93 HRDGLEAFTRFKTFSESENIEFWIACBDFPKSKGPGQIHLLKAKAIYEKFOTDAPKEVN 152				
Db	72 NSYGATLKFLRSEFSEENIEFWACEDFKITKNPLKMATKAKKIYEDFIQTGGPKEVN 131				
QY	153 LDPHIKVEITNSITPTLHSPPAASRVQLMEQDSYTFELKSDIYLDLWE 203				
Db	132 IDHFTKDVTLRNLVDLSSTFELAQSRIYTLMEKDSFGFLRSDDQVELCK 182				
RESULT 8					
Q7SZC6 PRELIMINARY; PRT; 208 AA.					
ID	Q7SZC6;				
AC	Q7SZC6;				
DT	01-OCT-2003 (TrEMBLrel. 25, Created)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Regulator of G-protein signaling 4.				
OS	Gallus gallus (Chicken).				

OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Psittacineae;
OC	Gallus.
OX	NCBI_TaxID=9031;
OX	{1}_TaxID=9031;
RN	SEQUENCE FROM N.A.
RP	TISSUED4 hindbrain;
RC	Grillet N., Dubreuil V., Dufour H., Goridis C., Brunet J.-F.;
RA	"Dynamic expression of RG84 in the developing nervous system and
RT	control by the paired-like homeoprotein Phox2b."
RI	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AV297457; AAP57222.1; ..
DR	EMBL; AV297457; AAP57222.1; ..
SQ	SEQUENCE 208 AA; 23523 MW; 838B31750FF0EA68 CRC64;
	Query Match 33.7%; Score 410.5; DB 13; Length 208;
	Best Local Similarity 45.2%; Pred. No. 1.3e-25;
	Matches 85; Conservative 38; Mismatches 56; Indels 9; Gaps 5;
QY	41 AKKENRSLVLVQKPEFHE-DTRSSRGHLAKETRVSPPEAVKWGESDKLLSHRDGLAA 99
	: : : : : : : : : : : : : : : : : :
Db	16 AKDMKRLGVLQLKSDSCDYGSSOGKEKYSSQRUSQEVEKKWAELENLIHHDRLAA 75
	: : : : : : : : : : : : : : : : : :
QY	100 FFRFLKTFESSENTIEFWIACDFKSKGPQIIHKAKAIYEKPIQTDPAPKEVNLDFTTKE 159
	: : : : : : : : : : : : : : : : : :
Db	76 PRAFPLKSYSEBNTIEFWVCSDEYKTKSPAKLSKARKTYDEFISVQATKEVNLDSCTRE 135
	: : : : : : : : : : : : : : : : : :
QY	160 VTINSITOPTLHPDAQSRVYQLMEODSTYRFLKSDIVLDMEGRRPOR---PTNLNR- 214
	: : : : : : : : : : : : : : : : : :
Db	136 KTSNHENPFTLSCDFDEQRKIFTLMEKDSYRFLKSP-VLDILVS--PPRAGCGPENCKEA 192
	: : : : : : : : : : : : : : : : : :
QY	215 RRSRFTCN 222
	: : : : : : : : : : : : : : : : : :
Db	193 HAHAALDCN 200
	: : : : : : : : : : : : : : : : : :

RESULT 9	Q925G9	PRELIMINARY;	PRT;	930 AA.
ID	Q925G9	PRELIMINARY;	PRT;	930 AA.
AC	Q925G9;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	PDZ-RGS3 protein.			
DE	RGS3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21197945; PubMed=11301003;			
RA	Lu Q., Sun E.E., Klein R.S., Flanagan J.G.;			
RT	"Ephrin-b reverse signaling is mediated by a novel PDZ-RGS protein and selectively inhibits G protein-coupled chemoattraction.";			
RL	Cell 105:63-79(2001).			
CC	-1- SIMILARITY: CONTAINS 1 RGS DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.			
DR	EMBL; AF350047; AAK38878.1; -.			
DR	MGD; MG1:1354734; Rgs3.			
DR	GO; GO:0005634; C:nucleus; IDA.			
DR	InterPro; IPR001478; PDZ.			
DR	InterPro; IPR00342; Regl_Gpotein.			
DR	Pfam; PF00595; PDZ; 1.			
DR	Pfam; PF00615; RGS; 1.			
DR	PRINTS; PR01301; RGS-PROTEIN.			
DR	ProDom; PD001580; Regl_Gpotein; 1.			
DR	SMART; SM00228; PDZ; 1.			
DR	SMART; SM00315; RGS; 1.			
DR	PROSITE; PSS0106; PDZ; 1.			
DR	PROSITE; PSS0132; RGS; 1.			
SQ	SEQUENCE 930 AA; 102511 MW; FB08CEA164D2F6A1 CRC64;			

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Best Local Similarity 45.3%; Pred.No. 1e-24;
Matches 82; Conservative 37; Mismatches 60; Indels 2; Gaps 1;

Qy 31 EYTSKEAIR--AKEVKNRLSLVQKPEFHEDTRSSRGHIAKETRVSPPEAVKNGESFD 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 748 DEASRKEKSNIAKDMKNKLAIFRRNESPGAQPAKSTDKTKTKFKPTSEALKWSESLE 807
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 89 KLSHRDGEAFTRFLKTEFSEENIEFWIACBDFPKSKGPOQIHLKAKAIYEFQTDAP 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 808 KLLHKYGLGVFOAFRTSEENIEFWIACBDFPKYKSKVAAKAKKIFAEFIAIQAC 867
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 149 KEVNLDPHTKEVITNSITOPTLHSDFAAQSRVYQVLMQSDSYTRFLKSDIYLDMEGRPQR 208
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 868 KEVNLDSYTREHTKENLQISITRGCFDLAQKRIFGLMEKDSYPRFLRSLDYLDLINQKMS 927
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 209 P 209
   |
Db 928 P 928

RESULT 10
Q864Z2 PRELIMINARY; PRT; 181 AA.
ID Q864Z2
AC Q864Z2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Regulator of G-protein signalling 5.
GN RGS5.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Weiss B., Hehlhans S.I., Wietelmann A.B., Zeyer A., Richter M.,
RA Kloevekorn W.P., Zimmermann R., von der Ahe D.;
RT "Differential gene expression in atherosclerotic coronary arteries.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DDbj databases.
DR EMBL; AJ549925; CAD71257.1; -.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPR000342; Regl_Gproteins.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
DR SEQUENCE 181 AA; 21054 MW; BEB98C7A4A99D669 CRC64;
SQ
Query Match 33.5%; Score 408.5; DB 6; Length 181;
Best Local Similarity 47.9%; Pred.No. 1.6e-25;
Matches 80; Conservative 36; Mismatches 48; Indels 3; Gaps 1;

Qy 40 RAKEKNRLSLVQKPEFHED--TRSSRGHIAKETRVSPPEAVKNGESFDKLSHRDG 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 15 RAKIKIKGLIKQKPEASVDLVIPIYNEKPDVPIQKPSLDEALQWRDLSLDKLLQNNYG 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 97 LEAFTRFLKTEFSEENIEFWIACBDFPKSKGPOQIHLKAKAIYEFQTDAPKEVNLDPFH 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 LASPKSLFKSEFSEENIEFWIACBDFPKYKSKVAAKAKKIEEFIOSEAPKEVNIHDF 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 157 TKEVITNSITOPTLHSDFAAQSRVYQVLMQSDSYTRFLKSDIYLDLME 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 135 TREITMKNLVEPSSFDVAKRIYALMEKDSYPRFVSEFQEFIK 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
Q8EXT1 PRELIMINARY; PRT; 180 AA.
ID Q8EXT1
AC Q8EXT1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

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01-JUN-2003 (Tremblrel. 24, Last annotation update)
Regulator of G-protein signaling 8.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Retina;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nuclei 420:563-573(2002).
EMBL; AK044337; BAC1874.1; -.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPR000342; Regl_Gpotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gpotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
SQ SEQUENCE 180 AA; 20963 MW; 00FC35E572785856 CRC64;

Query Match 33.3%; Score 405.5; DB 11; Length 180;
Best Local Similarity 47.1%; Pred. No. 2.7e-25;
Matches 81; Conservative 31; Mismatches 55; Indels 5; Gaps 2;

QY 40 RAKEXRNLRLSLVQKPEPHEDTRSRSGHLAKETRVSPPEAVKMGESFDKLLSRDG 96
D 9 RKNKGRTRGLCLSHKSDSCSFTAILPDKPNRALK--RLSTEETRAWGESFDVLLSHKYG 66
QY 97 LEATFRFLKTEFSEENIEFWIACEDFKKSGPQIHLKAKAIYKFIQTDPAPKEVNDHF 156
D 67 VAAPFAFLKTEFSEENIEFWIACEDFKKSGPQIHLKAKAIYKFIQTDPAPKEVNDHF 126
QY 157 TKEVITNSITOPTLHSDAASRVVQVMEQDSYTRFLKSDIYLDIMEGRPQR 208
D 127 TREATKKNQPSLTCTDPAQGVHSLMEKDSYRFLRSKMYLLDSQQR 178

RESULT 12
Q8NFN4 PRELIMINARY; PRT; 917 AA.
AC Q8NFN4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE RGS3 isoform PDZ-RGS3.
GN RGS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22032988; PubMed=12036301;
RA Kehrl J.H., Srikumar D., Harrison K., Wilson G.L., Shi C.S.;
RT "Additional 5' Exons in the RGS3 Locus Generate Multiple mRNA
Transcripts, One of Which Accounts for the Origin of Human PDZ-RGS3.";
RL Genomics 79:860-868(2002).
CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
CC EMBL; AF490840; AAM33255.1; -.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00595; PDZ; 1.
DR ProDom; PD001580; Regl_Gpotein.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gpotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
SQ SEQUENCE 917 AA; 100975 MW; 3347CFD383BFABF9 CRC64;

Query Match 33.2%; Score 404; DB 4; Length 917;
Best Local Similarity 44.2%; Pred. No. 2.5e-24;
Matches 80; Conservative 39; Mismatches 60; Indels 2; Gaps 1;

QY 31 EETSKEAKIR--AKEKNRNLRLSLVQKPEPHEDTRSRSGHLAKETRVSPPEAVKMGESFD 88
D 735 DEASRRKSKNLAKOMKNKLGIFRRNESPGAPGAKADKMKSKFPTSEALKWGESLE 794
QY 89 KLLSHRDGLEAFTRFLKTEFSEENIEFWIACEDFKKSGPQIHLKAKAIYKFIQTDP 148
D 795 KLLVHKYGLAVFOAFLRTEFSEENIEFWIACEDFKKSGPQIHLKAKAIYKFIQTDP 854
QY 149 KEVNLDFHTKEVITNSITOPTLHSDAASRVVQVMEQDSYTRFLKSDIYLDIMEGRPQR 208
D 855 KEVNLDSYTRHTKONLQSVTRGCFDLAKRIFGLMEKDSYRFLRSKMYLLDSQQR 914
QY 209 P 209
D 915 P 915

RESULT 13
Q8WXA0 PRELIMINARY; PRT; 917 AA.
AC Q8WXA0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE PDZ-RGS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chatterjee T.K., Fisher R.A.;
RT "Human PDZ-RGS3.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR EMBL; AF463495; AAL68829.1; -.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000342; Regl_Gpotein.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gpotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
SQ SEQUENCE 917 AA; 100975 MW; 3347CFD383BFABF9 CRC64;

Query Match 33.2%; Score 404; DB 4; Length 917;
Best Local Similarity 44.2%; Pred. No. 2.5e-24;
Matches 80; Conservative 39; Mismatches 60; Indels 2; Gaps 1;

QY 31 EETSKEAKIR--AKEKNRNLRLSLVQKPEPHEDTRSRSGHLAKETRVSPPEAVKMGESFD 88
D 735 DEASRRKSKNLAKOMKNKLGIFRRNESPGAPGAKADKMKSKFPTSEALKWGESLE 794
QY 89 KLLSHRDGLEAFTRFLKTEFSEENIEFWIACEDFKKSGPQIHLKAKAIYKFIQTDP 148
D 795 KLLVHKYGLAVFOAFLRTEFSEENIEFWIACEDFKKSGPQIHLKAKAIYKFIQTDP 854
QY 149 KEVNLDFHTKEVITNSITOPTLHSDAASRVVQVMEQDSYTRFLKSDIYLDIMEGRPQR 208
D 855 KEVNLDSYTRHTKONLQSVTRGCFDLAKRIFGLMEKDSYRFLRSKMYLLDSQQR 914
QY 209 P 209
D 915 P 915
```

QY 149 KEVNLDFTHTKEVITNSITQPTLHSDFAAQSRYVQLMEQDSYTRFLKSDIYLDLMEGRPQR 208
 DB 855 KEVNLDSTYREHTKONLQSVTRGCFDLAQKIFGLMEKDSYPRFLRSDLYLDLQNKMS 914

QY 209 P 209
 DB 915 P 915

RESULT 14
 Q8IUQ1 PRELIMINARY; PRT; 917 AA.
 AC Q8IUQ1;
 DT 01-WAR-2003 (TRENBLrel. 23, Created)
 DT 01-WAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Regulator of G-protein signalling 3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC042555; AAH42555.1; -.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR000342; Regl_Gpotein.
 DR Pfam; PF00595; PDZ; 1.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 DR ProDom; PD001580; Regl_Gpotein; 1.
 DR SMART; SM00228; PDZ; 1.
 DR PROSITE; PS50106; PDZ; 1.
 DR PROSITE; PS50132; RGS; 1.
 DR PROSITE; PS50132; RGS; 1.
 SQ SEQUENCE 917 AA; 100920 MW; AEBBC3427BC2BC14 CRC64;

Query Match 33.2%; Score 404; DB 4; Length 917;
 Best Local Similarity 44.2%; Pred. No. 2.5e-24;
 Matches 80; Conservative 39; Mismatches 60; Indels 2; Gaps 1;

QY 31 ETSKEAKIR--AKEKRNRLSLVQKPEFHEDTRSRSGHLAKETRVSPPEAVKWSGFD 88
 DB 735 DEASRKRSKNLAKDMKNKLGIFRRNESPGAPPAGKADKMKSKFPTSEALKWGESLE 794

QY 89 KLLSHRDGLEAFTRFLKTEFSEENIEFWIACEDPKKSGPOQIHLKAKAIYEKFIQTDP 148
 DB 795 KLLVHKYGLAVFQAFRTFSEENLEFWIACEDPKKVKSQSKASKAKKIFAETIAIQC 854

QY 149 KEVNLDFTHTKEVITNSITQPTLHSDFAAQSRYVQLMEQDSYTRFLKSDIYLDLMEGRPQR 208
 DB 855 KEVNLDSTYREHTKONLQSVTRGCFDLAQKIFGLMEKDSYPRFLRSDLYLDLQNKMS 914

QY 209 P 209
 DB 915 P 915

RESULT 15
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 AC Q8NFNS;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE RGS3 isoform C2PA-RGS3.
 GN RGS3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22032988; PubMed=12036301;
 RA Kehrl J.H., Srikumar D., Harrison K., Wilson G.L., Shi C.S.;
 RT "Additional 5' Exons in the RGS3 Locus Generate Multiple mRNA
 Transcripts, One of Which Accounts for the Origin of Human PDZ-RGS3.";
 RL Genomics 79:860-868(2002).
 CC -1- SIMILARITY: CONTAINS 1 RGS DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
 DR EMBL; AF490839; AA03254.1; -.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR008973; C2_CaLb.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR000342; Regl_Gpotein.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00595; PDZ; 1.
 DR Pfam; PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 DR ProDom; PD001580; Regl_Gpotein; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00228; PDZ; 1.
 DR SMART; SM00315; RGS; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS50106; PDZ; 1.
 DR PROSITE; PS50132; RGS; 1.
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 SQ SEQUENCE 1093 AA; 120970 MW; B211E7E5643436B CRC64;

Query Match 33.2%; Score 404; DB 4; Length 1093;
 Best Local Similarity 44.2%; Pred. No. 3.1e-24;
 Matches 80; Conservative 39; Mismatches 60; Indels 2; Gaps 1;

QY 31 ETSKEAKIR--AKEKRNRLSLVQKPEFHEDTRSRSGHLAKETRVSPPEAVKWSGFD 88
 DB 911 DEASRKRSKNLAKDMKNKLGIFRRNESPGAPPAGKADKMKSKFPTSEALKWGESLE 970

QY 89 KLLSHRDGLEAFTRFLKTEFSEENIEFWIACEDPKKSGPOQIHLKAKAIYEKFIQTDP 148
 DB 971 KLLVHKYGLAVFQAFRTFSEENLEFWIACEDPKKVKSQSKASKAKKIFAETIAIQC 1030

QY 149 KEVNLDFTHTKEVITNSITQPTLHSDFAAQSRYVQLMEQDSYTRFLKSDIYLDLMEGRPQR 208
 DB 1031 KEVNLDSTYREHTKONLQSVTRGCFDLAQKIFGLMEKDSYPRFLRSDLYLDLQNKMS 1090

QY 209 P 209
 DB 1091 P 1091

Search completed: August 20, 2004, 16:47:00
 Job time : 78.5 secs

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OM nucleic - nucleic search, using sw model
Run on: August 20, 2004, 03:13:58 ; Search time 4611.24 Seconds
(without alignments)
10940.929 Million cell updates/sec
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Perfect score: 1164
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				GenEmbl:			
1:	gb	ba:	*	1:	gb	ba:	*
2:	gb	htg:	*	2:	gb	htg:	*
3:	gb	in:	*	3:	gb	in:	*
4:	gb	in:	*	4:	gb	in:	*
5:	gb	ov:	*	5:	gb	ov:	*
6:	gb	pat:	*	6:	gb	pat:	*
7:	gb	ph:	*	7:	gb	ph:	*
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9:	gb	pr:	*	9:	gb	pr:	*
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13:	gb	un:	*	13:	gb	un:	*
14:	gb	vi:	*	14:	gb	vi:	*
15:	em	ba:	*	15:	em	ba:	*
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17:	em	hum:	*	17:	em	hum:	*
18:	em	in:	*	18:	em	in:	*
19:	em	mu:	*	19:	em	mu:	*
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32:	em	htg_other:	*	32:	em	htg_other:	*
33:	em	htg_mus:	*	33:	em	htg_mus:	*
34:	em	htg_pln:	*	34:	em	htg_pln:	*
35:	em	htg_rod:	*	35:	em	htg_rod:	*
36:	em	htg_mam:	*	36:	em	htg_mam:	*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1164	100.0	1164	6	AR165091	Sequence
2	1164	100.0	1164	6	BD265699	RGS-conta
3	1164	100.0	1164	6	AR214936	Sequence
4	1113.2	95.6	1937	10	AB042807	Mus muscu
5	1104.4	94.9	1399	10	AF302685	Mus muscu
6	601	51.6	2136	9	AK057114	Homo sapi
7	601	51.6	2164	9	BC020632	Homo sapi
8	599.6	51.5	1840	6	AX299975	Sequence
9	599.6	51.5	2144	6	AX299976	Sequence
10	599.6	51.5	2144	6	AF268036	Homo sapi
11	597.8	51.4	2138	9	AF076642	Homo sapi
12	596	51.2	2217	6	AR165090	Sequence
13	596	51.2	2217	6	BD265698	RGS-conta
14	596	51.2	2217	6	AR214935	Sequence
15	535.4	46.0	218670	10	AC102163	Mus muscu
16	352.2	30.3	110000	2	AC112625_1	Continuation (2 of
17	227.4	19.5	94175	9	AL513175	Human DNA
18	227.4	19.5	107919	2	AL391274	Homo sapi
19	208.8	17.9	302893	2	AC124876	Rattus no
20	192.2	16.5	1486	6	AX299963	Sequence
21	177.6	15.3	241	6	AX299968	Sequence
22	156.4	13.4	1463	5	AF502148	Gallus ga
23	156.4	13.4	1517	5	AF502149	Gallus ga
24	156.2	13.4	737	10	AF215668	Mus muscu
25	156.2	13.4	1354	10	BC023001	Mus muscu
26	156.2	13.4	1364	10	AF432916	Mus muscu
27	154.6	13.3	1240	10	MMU67187	Mus musculu
28	154	13.2	494	4	AF472577	Ovis arie
29	152.8	13.1	2765	5	BC054594	Danio rer
30	152.4	13.1	636	9	AF493926	Homo sapi
31	152.4	13.1	636	9	BT007065	Homo sapi
32	152.4	13.1	636	12	BT008081	Synthetic
33	152.4	13.1	685	10	AF321837	Rattus no
34	152.4	13.1	1345	6	AR270715	Sequence
35	152.4	13.1	1345	6	AR380698	Sequence
36	152.4	13.1	1345	6	AX663626	Sequence
37	152.4	13.1	1345	9	HUMGOS8PFC	Human helix
38	152.4	13.1	1363	10	AY043246	Rattus no
39	152.4	13.1	1377	9	BC007049	Homo sapi
40	152.4	13.1	1458	10	BC061969	Rattus no
41	152.4	13.1	1629	10	AF279918	Rattus no
42	150.2	12.9	408	6	AX710064	Sequence
43	144.4	12.4	2342	9	AB066513	Macaca fa
44	143.6	12.3	540	6	AX300745	Sequence
45	143.6	12.3	543	9	AF300649	Homo sapi

ALIGNMENTS

RESULT 1	AR165091	AR165091	Sequence 3 from patent US 6274362.	1164 bp	DNA	linear	PAT 17-OCT-2001
LOCUS	AR165091	Sequence 3 from patent US 6274362.					
DEFINITION	AR165091	Sequence 3 from patent US 6274362.					
ACCESSION	AR165091	Sequence 3 from patent US 6274362.					
VERSION	AR165091.1	GI:16238488					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1164)						
AUTHORS	Hodge,M.R., and Yowe,D.						
TITLE	RGS-containing molecules and uses thereof						
JOURNAL	Patent: US 6274362-A 3 14-AUG-2001;						
FEATURES	Location/Qualifiers						

241	Db	GGCCAAAATCAGAGCGAAAGAAAAAGGAATAGACTAAGTCTTCTCCTCAGAGGCTGA	300
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301	Db	CTTCCATGGAGAGACTCAAGCCAGTAGACTCTGCCCTCTTGGCCAAAGAAACAAGAGTCTC	360
361	Qy	TCCTGAAGAAGCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCTCATAGATGG	420
361	Db	TCCTGAAGAAGCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCTCATAGATGG	420
421	Qy	AGTGGATGCTTTTACCCAGATTCTTAAACCTGAATTCAGTGAGGAGAAACATTCGAAATTTG	480
421	Db	AGTGGATGCTTTTACCCAGATTCTTAAACCTGAATTCAGTGAGGAGAAACATTCGAAATTTG	480
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481	Db	GGTCGCCCTGTCAAGACTTCAAGAAATCAAGGAACCTCAACAAATCATCTTAAAGCAAA	540
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1081	Qy	TATTTCTACAATAACAGTCAGTAAGAAGAGCTTTGAAGCCGAATTCGAGCACACTGGG	1140
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1141	Qy	GCCGGTACTAGTGGATCCGAGCTC	1164
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RESULT 3					
AR214936					
LOCUS	AR214936	1164 bp	DNA	linear	PAT 25-SEP-2002
DEFINITION	Sequence 3 from patent US 6410240.				
ACCESSION	AR214936				
VERSION	AR214936.1	GI:23312889			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				

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LOCUS	AB042807	1937 bp mRNA linear	ROD 12-JUN-2001
DEFINITION	Mus musculus RGS mRNA, complete cds.		
ACCESSION	AB042807		
VERSION	AB042807.1	GI:14349231	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
TITLE	1 (sites)		
JOURNAL	Nagata, Y., Oda, M., Nakata, H., Shozaki, Y., Kozasa, T. and Todokoro, K.		
MEDLINE	A novel regulator of G-protein signaling bearing GAP activity for		
PUBMED	Galphai and Galphag in megakaryocytes		
AUTHORS	Blood 97 (10), 3051-3060 (2001)		
TITLE	21240406		
JOURNAL	11342430		
REFERENCE	2 (bases 1 to 1937)		
AUTHORS	Todokoro, K., Nagata, Y. and Oda, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-MAY-2000) Kazuo Todokoro, RIKEN Tsukuba Institute,		
REFERENCE	Molecular Cell Science Laboratory, Koyadai, Tsukuba, Ibaraki		
305-0074, Japan (E-mail: todokoro@rtc.riken.go.jp,			
Tel: 81-298-36-9075, Fax: 81-298-36-9090)			
Location/Qualifiers			
1. .1937			
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FLKTFEENIEEHWACEDEKCKEPOQIILKALYKPFQNDAPKEVNIIDPHTKEV			
IAKSIADPTLHSDTASRYQLMEHDSYKRFKSLYLLIEGRFQRPDNLRRRS			
FTINDQDVDSVAIWL"			
gene			
CDS			
Query Match	95.6%;	Score 1113.2;	DB 10;
Best Local Similarity	99.7%;	Pred. No. 1.3e-194;	Length 1937;
ORIGIN			

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Db	63	TTTTTGTAAAGAAATCTGAGGAAAGATTCGGGATAGCGCTTTATTCAGAGATGTTTCCT								122
QY	61	ATGAAATAGCATTCATCTGTGGGAGAGAGAAAGACTTAAGGAAATCTGACATCTGTTGGTC								120
Db	123	ATGAAACAGCATTCATCTGTGGGAGAGAGAAAGACTTAAGGAAATCTGACATCTGTTGGTC								182
QY	121	ACTGGGACAGATATGATGTCCTGTTTCTCTCTCAATTAATATATGTCGATC								180
Db	183	ACTGGGACAGATATGATGTCCTGTTTCTCTCTCAATTAATATATGTCGATC								242
QY	181	AAAAGAGAAATCTTTTCAAACTAATGATGCGGTGAGGAAAGAAAGAAACAGCATCGA								240
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Db	423	TCTGAAGAGCAGTGAATGGCTGAATCATTTGACAAATTCCTCTCATAGAGATGG								482
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Db	603	GGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTAAACATTTTCA								662
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Db	663	TACTAAAGAAATTAATTCCTAAGAGCATCGCCAGCCCACTCTCCACAGTTTGTATCGGC								722
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QY	901	CTAATGTGCTACTTCTTAAATATAGCTTGTGTATAGAGAGATGATTTCAATTTTAAAT								960
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QY	961	ACACCATGCAATACATATTAATTAAGACTTTTATATATATATACTAAATATATCATC								1020
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QY	1021	ATCTATCTTCCGAATATTTTATGAATCTATCTGATATCTATCTAATAAATATCTT								1080
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AF302685			
AF302685.1 GI:12407842			
Mus musculus (house mouse)			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
REFERENCE			
1 (bases 1 to 1399)			
Park,I.K., Klug,C.A., Li,K., Jerabek,L., Li,L., Nanamori,M., Neubig,R.R., Hood,L., Weissman,I.L. and Clarke,M.F.			
TITLE			
Molecular cloning and characterization of a novel regulator of G-protein signaling from mouse hematopoietic stem cells			
J. Biol. Chem. 276 (2), 915-923 (2001)			
JOURNAL			
MEDLINE			
PUBMED			
11042171			
REFERENCE			
2 (bases 1 to 1399)			
Park,I.K., Klug,C.A., Li,K., Jerabek,L., Li,L., Nanamori,M., Neubig,R.R., Hood,L., Weissman,I.L. and Clarke,M.F.			
TITLE			
Direct Submission			
JOURNAL			
Submitted (04-SEP-2000) Internal Medicine, University of Michigan, 1500 E. Medical Center Dr., Ann Arbor, MI 48109, USA			
FEATURES			
Location/Qualifiers			
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Matches 1116; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
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QY	121	ACTGGGACAGAAATATGGATATGTCATGGTTTCTCTCTCAATTAATATATGTGTAATC	180
Db	174	ACTGGGACAGAAATATGGATATGTCATGGTTTCTCTCTCAATTAATATATGTGTAATC	233
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Db	234	AAAAGAGAAACCTTTTTCACCTAATGTCATGGTTCAGGGAAGAGAAACCAAGCATCGA	293
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QY	294	GGCCAAAATCAGACCGGAAAGAAAAAGGAATAGACTGTTCTCTCCTACAGAGGCTCGA	353
Db			

Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K., Masuko, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

2 (bases 1 to 2136)
Isogai, T., Otsuki, T. and Sugiyama, T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

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ORIGIN

Query Match 51.6%; Score 601; DB 9; Length 2136;
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Matches 816; Conservative 0; Mismatches 235; Indels 34; Gaps 4;

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QY 60 TATGAATAGCATTCATCTGCGGAGAGAGAGACTAAGNAATCTGACATCTGTGGT 119
DB 98 TATGAATAGTATTATTAATGAATAGTAGGAAGATGTAATAATAGACATCTTCAT 157
QY 120 CACTGGGACAGAAATATGGATATGTCACCTGGTTCCTCTCAATTAATATGTCGAAT 179
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QY 300 ACTTCCTGAGAGACTCAAGCAGTATGATCGCTTGGCCAAAGAAACAAGAGTCT 359
DB 336 AGTTTCATGAAGACACCCGCTCCAGTAGATCGGCACTTGGCCAAAGAAACAAGAGTCT 395
QY 360 CTCCTGAAGAGACAGTGAATGGCTGAATCATTTGACAAATTCCTCTCATAGAGATG 419
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DB 456 GACTAGAGGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAAATATTTGAATTT 515
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DB 516 GATAGCTGTGAAGATTCAGAAAGCAAGGAGACCTCACAATTCACCTTAAAGCAA 575
QY 540 AGGCAATCTAGAGAAATTCATTGCAATGATGCCCCCAAGAGGTTTAACTGATTTTC 599

DB 576 AAGCAATATATGAGAAATTTATACAGACTGATGCCCAAGAGAGTTAACTTGATTTTC 635
QY 600 ATACTAAGAAGTAATTCGTAAGAGCATGCCCGAGCCCACTCTCCACAGTTTGTACCG 659
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QY 720 AGACCTTACTTACATTTGATAGAGGAGAGCCTCAGAGACCAACAACCTTAGGACGAT 779
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QY 840 GAGTAAAGTCATTTCTCTTTCATAGTGTATGATGTAATCTTAAATATATACTAAT 899
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QY 900 ACTAATGTGTACTTCTAAATATATAGCTTGTGTATAGAGAGATGATTTTCAATTT----- 954
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RESULT 7
BC020632 2164 bp mRNA linear PRI 04-OCT-2003
LOCUS Homo sapiens regulator of G-protein signalling 18, mRNA (cdna clone MGC:22266 IMAGE:4714909), complete cds.
DEFINITION BC020632
ACCESSION BC020632.1 GI:18088322
VERSION MGC.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2164)
AUTHORS Klausner, R.D., Collins, E.A., Grouse, L.H., Derge, J.G., Strausberg, R.L., Feingold, E.A., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

TITLE

JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	Db	157	T--TTAGAGAGATGGAAACAATCTGCTTTCTTTCTCAATAATATGTGTGAAT	214
MEDLINE	22388257				
PUBMED	12477932	Qy	180	CAAAAGAGAAAACTTTTTCAAACTAATGATGGGTACGGGAAAGAGAAACAAGCATCG	239
REFERENCE	2 (bases 1 to 2164)				
AUTHORS	Strausberg, R	Db	215	CAAAAGAGAAAACTTTTTCAAAGTAAATACATGGTTCAGGAAAAGAGAAACAAGCAAG	274
TITLE	Direct Submission				
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian	Qy	240	AGCCCAAAATCAGAGCGAAGAAAAGAAAGAAATAGACTAAGTCTCTCTTACAGAGCCCTG	299
	Gene Collection (MGC), Cancer Genomics Office, National Cancer	Db	275	AGCCCAAAATCAGAGCTAAGGAAAAGAAATAGACTAAGTCTCTCTTGGCAGAAACCTG	334
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,				
	USA	Qy	300	ACTTCCATGGAGAGACTCAAGCCAGTAGATCGCCCTCTTGGCCAAAGAAAACAAGAGTCT	359
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	Db	335	AGTTTCATGAAGACACCCGCTCCAGTAGATCTGGGCACITGGCCAAAGAAAACAAGAGTCT	394
COMMENT	Contact: MGC help desk				
	Email: cgapbs-remail.nih.gov	Qy	360	CTCCTGAAGAGCAGTGAATGGCTGAATCAATTTGACAAAATGCTCTCTCTCATAGAGATG	419
	Tissue Procurement: CLONTECH	Db	395	CCCTGAAGAGGCGAGTGAATGGGTGAATCATTTTGACAAACCTGCTTCCCATAGAGATG	454
	cDNA Library Preparation: CLONTECH Laboratories, Inc.	Qy	420	GAGTGATGCTTTTACAGATTTCTTAAACCTGAATTCAGTGAGGAGAAACATTTGATTTT	479
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)	Db	455	GACTAGAGGCTTTTACAGATTTCTTAAACCTGAATTCAGTGAGGAGAAATTTGATTTT	514
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome	Qy	480	GGTCCCTGTGAAGACTTCAAGAAATGCAAGAACCTCAACAATCATCTCTTAAAGCAA	539
	Center, Stanford University School of Medicine, Stanford, CA 94305	Db	515	GGATAGCCTGTGAAGATTTCAAGAAAAGCAAGGACCTCAACAATTCACCTTAAAGCAA	574
	Web site: http://www-sbgc.stanford.edu	Qy	540	AGCATCTATGAGAAATTCATTCAGAATGATGCCCCCAAGAGGTTAAACATTTGATTTT	599
	Contact: (Dickson, Mark) mcd@paxil.stanford.edu	Db	575	AGCATATATGAGAAATTTTATACAGATGATGCCCCCAAGAGGTTAAACATTTGATTTT	634
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,	Qy	600	ATACTAAAGAGTAATTTGCTAAGAGATCGCCAGCCCACTCTCCACAGTTTGTATACGG	659
	R. M.	Db	635	ACAAAAAGAGTCATTACAAAACAGCATCACTCAACCTACCCCTCCACAGTTTGTATGCTG	694
FEATURES	Clone distribution: MGC clone distribution information can be found	Qy	660	CACAAAGCAGAGTGTACCGACTCATCGAACATGACAGATTATAACCGCTTTTGAATCTCG	719
source	through the I.M.A.G.E. Consortium/ILLNL at: http://image.llnl.gov	Db	695	CACAAAGCAGAGTGTATCAGCTCATGGAACAAGACAGTTATACACGTTTCTGAAATCTG	754
	Series: IRL Plate: 37 Row: d Column: 18				
	This clone was selected for full length sequencing because it	Qy	720	AGACCTACTTACATTTTGTATAGAGAGACCTCAGAGACCAACAAACCTTAGGAGACGAT	779
	passed the following selection criteria: matched mRNA gi: 18640749.	Db	755	ACATCTATTAGACTTTGATGGAAGAGACCTCAGAGACCAACAATCTTAGGAGACGAT	814
	Location/Qualifiers	Qy	780	CAGATCATTTTACTTCAATGATTTCCAGATGTAAGTCAGATGTTGCCATTTGGTTAT	839
	1. .2164	Db	815	CAGCTCAITTTACCTGCAATGAATTCGAAGATGTAACAATCAGACGTTGCCATTTGGTTAT	874
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	DNA				
	linear				
	PAT 26-NOV-2001				

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VERSION      AX299975.1  GI:17129462
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Murray,D.L. and Gagnon,A.W.
AUTHORS      Nucleic acids encoding a novel regulator of G protein signaling,
TITLE        rgs18, and uses thereof
JOURNAL      Patent: WO 0183514-A 18 08-NOV-2001;
              Aventis Pharmaceuticals Products Inc. (US)
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Query Match      51.5%; Score 599.6; DB 6; Length 1840;
Best Local Similarity 75.2%; Pred. No. 2.5e-100;
Matches 814; Conservative 0; Mismatches 234; Indels 34; Gaps 4;

QY 4 TTGTAAAGAAAATCTGAGAAAGATTCGGGATAGCGCTTTATTC-AGGATGTTTTCTCTAT 62
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QY 543 CAATCTATGAGAAATTCATTCAGATATGATGCCCCCAAGAGGTTAAACATTCATTTTCATA 602
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DB 1087 TC 1088

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LOCUS         Sequence 19 from Patent WO0183514.
DEFINITION    AX299976
ACCESSION     AX299976
VERSION       AX299976.1  GI:17129463
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Murray,D.L. and Gagnon,A.W.
TITLE         Nucleic acids encoding a novel regulator of G protein signaling,
              rgs18, and uses thereof
JOURNAL       Patent: WO 0183514-A 19 08-NOV-2001;
              Aventis Pharmaceuticals Products Inc. (US)
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Query Match      51.5%; Score 599.6; DB 6; Length 2144;
Best Local Similarity 75.2%; Pred. No. 2.5e-100;
Matches 814; Conservative 0; Mismatches 234; Indels 34; Gaps 4;

QY 4 TTGTAAAGAAAATCTGAGAAAGATTCGGGATAGCGCTTTATTC-AGGATGTTTTCTCTAT 62
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DB 94 GGAATAGTATTAAATGAAGTGTGATAAGGAGGATGTAATAATTAGACATCTCTCAT 151
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DB 152 TTAGAGAGAAGATGGAAAACAATTCGCTTTCTTTCTCAATAAATATGTGTGAATCAA 211
QY 183 AAGAGAAAATCTTTTTCAAAACCTAATGCGATGGGTTCAGGGAAGAAAGAAACAAGCATCGAGG 242
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RESULT 10
 AF268036
 LOCUS
 DEFINITION Homo sapiens regulator of G-protein signaling 18 mRNA, complete cds.
 ACCESSION AF268036
 VERSION AF268036.1 GI:14279410
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2144)
 AUTHORS Gagnon,A.W., Murray,D.L. and Leadley,R.J. Jr.

TITLE Cloning and characterization of a novel regulator of G protein signalling in human platelets
 JOURNAL Cell. Signal. 14 (7), 595-606 (2002)
 MEDLINE 21952499
 PUBMED 11955952
 REFERENCE 2 (bases 1 to 2144)
 AUTHORS Gagnon,A.W., Murray,D.L. and Leadley,R.J. Jr.
 TITLE Direct Submission
 JOURNAL Submitted (16-MAY-2000) Pfizer Central Research, Eastern Point Rd, Groton, CT 06340, USA
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 Query Match 51.5%; Score 599.6; DB 9; Length 2144;
 Best Local Similarity 75.2%; Pred. No. 2.5e-100;
 Matches 814; Conservative 0; Mismatches 234; Indels 34; Gaps 4;
 Qy 4 TTGTAGAAAAAATCTGAGGAAAGATTCTGGATAGCGCTTTTATTC-AGGATGTTTCTAT 62
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 RESULT 11
 AF076642
 LOCUS
 DEFINITION Homo sapiens regulator of G-protein signaling 13 mRNA, complete cds.
 ACCESSION AF076642
 VERSION AF076642.1 GI:8885627
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2138)
 Zhang, W., Wan, T., Yuan, Z., He, L. and Cao, X.
 A novel regulator of G-protein signaling
 Unpublished
 2 (bases 1 to 2138)
 Zhang, W., Wan, T., Yuan, Z., He, L. and Cao, X.
 Direct Submission
 Submitted (07-JUL-1998) Department of Immunology, Shanghai
 Brilliance Biotechnology Institute & Second Military Medical
 University, 800 Xiangyin Road, Shanghai 200433, P.R. China
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 Best Local Similarity 74.6%; Pred. No. 5.3e-100;
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Db 1076 C 1076

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LOCUS ARI65090 2217 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6274362.
ACCESSION ARI65090
VERSION ARI65090.1 GI:16238486
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2217)
AUTHORS Hodge,M.R. and Yowe,D.
TITLE RGS-containing molecules and uses thereof
JOURNAL Patent: US 6274362-A 1.14-AUG-2001;
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BD265698
LOCUS 2217 bp DNA linear PAT 17-JUL-2003
DEFINITION RGS-containing molecules and uses thereof.
ACCESSION BD265698
VERSION BD265698.1 GI:33075466
KEYWORDS JP 2002535979-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2217)
AUTHORS Hodge,M.R. and Yowe,D.
TITLE RGS-containing molecules and uses thereof
JOURNAL Patent: JP 2002535979-A 1 29-OCT-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002535979-A/1
PD 29-OCT-2002
PF 04-FEB-2000 JP 2000597306
PR 04-FEB-1999 US 09/244314
PI MARTIN R HODGE, DAVID YOWE
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/02, PC
C12Q1/68,
PC G01N33/53,G01N33/566,C12N15/00,C12N5/00,C12N5/00 CC
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Best Local Similarity 75.8%; Pred. No. 1.1e-99;

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 ACCESSION AC102163
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 KEYWORDS HTG.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 218670)
 Birren,B., Nusbaum,C. and Lander,E.
 Mus musculus chromosome 1, clone RP23-431N20
 Unpublished
 2 (bases 1 to 218670)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Bouckhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Kanat,A., Karatas,A., Kells,C., LaRoque,K.,
 Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
 Meneus,L., Minova,T., Mienna,V., Murphy,T., Naylor,J., Nguyen,C.,
 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL Direct Submission
 REFERENCE Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 218670)
 REFERENCE
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavskiy,L., Bouckhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
 Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K.,
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,

Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
 Graham,L., Grand-Pierre,N., Hagos,B., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
 Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C.,
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
 Meldrim,J., Meneus,L., Minova,T., Mienna,V., Murphy,T., Naylor,J.,
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
 Rachupka,A., Ramasamy,U.A., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (21-OCT-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 218670)
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
 Boguslavskiy,L., Bouckhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
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 Submitted (06-NOV-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Nov 6, 2003 this sequence version replaced gi:37777395.
 All repeats were identified using RepeatMasker:
 Snit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L18154

Center clone name: 431_N20

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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XX
DT 04-DEC-2000 (first entry)
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KW RGS; regulators of G-protein signaling; GTPase activating protein; GAP;
KW G-alpha protein; cell adhesion; chemotaxis; vulnery; immunosuppressor;
KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;
KW cytostatic; hepatotropic; anti-anaemic; modulator; gene therapy; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 134..841
FT /tag= a
FT /product= "RGS_protein"
XX
PN WO200046236-A2.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-US002977.
XX
PR 04-FEB-1999; 99US-00244314.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Hodge MR, Yowe D;
XX
DR WPI; 2000-532893/48.
DR P-PSDB; AA971154.
XX
PT Novel regulator of G-protein signaling nucleic acids and polypeptides,
PT useful as diagnostic and investigative tools and to treat G-protein
PT signaling disorders.
XX
PS Claim 1; Page 102-104; 105pp; English.
XX
CC The RGS (regulators of G-protein signaling) protein genes, clones
CC AAH16395 and m1975, were identified in human and murine spleen cDNA
CC libraries, respectively. Both proteins have unique N- and C-terminal

CC sequences. The C-terminal location of the RGS domain is consistent with
 CC RGSs known to act as G-protein activating proteins (GAPs) for G-alpha
 CC proteins. G-alpha-i linked receptors support rapid adhesion and directed
 CC migration of leukocytes and other cell types. The novel RGS proteins may
 CC be used to modulate cell adhesion and chemotaxis, e.g. for aiding wound
 CC repair. The RGS proteins, related cDNAs and anti-RGS antibodies are
 CC useful for modulation, diagnosis and treatment of immune and respiratory
 CC disorders

XX SQ Sequence 1164 BP; 406 A; 202 C; 222 G; 334 T; 0 U; 0 Other;

Query Match 100.0%; Score 1164; DB 3; Length 1164;
 Best Local Similarity 100.0%; Pred. No. 4.7e-246;
 Matches 1164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGTAGAAAAATCTGAGAAAGATTCGGATAGCGCTTTTATTCAGAGATGTTTCT 60
 DB 1 TTTTGTAGAAAAATCTGAGAAAGATTCGGATAGCGCTTTTATTCAGAGATGTTTCT 60
 QY 61 ATGAATAGCATCTCTGTGGGAGAGAGAGACTAAGAAATCTGACATCTGTGGTC 120
 DB 61 ATGAATAGCATCTCTGTGGGAGAGAGAGACTAAGAAATCTGACATCTGTGGTC 120
 QY 121 ACTGGGACAGATATGGATATGTCATGCTGTTTCTCTCAATTAATATGTTGAATC 180
 DB 121 ACTGGGACAGATATGGATATGTCATGCTGTTTCTCTCAATTAATATGTTGAATC 180
 QY 181 AAAAGAGAAACTTTTTCAAATTAATGATGGGTGAGGAAAGAAAGAAAGCAATCGA 240
 DB 181 AAAAGAGAAACTTTTTCAAATTAATGATGGGTGAGGAAAGAAAGAAAGCAATCGA 240
 QY 241 GSCCAATCAGAGCGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 300
 DB 241 GSCCAATCAGAGCGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 300
 QY 301 CTTTCATGAGAGACTCAAGCCAGTAGATCTGCTTGGCCAAAGAAAGAAAGAGTCTC 360
 DB 301 CTTTCATGAGAGACTCAAGCCAGTAGATCTGCTTGGCCAAAGAAAGAAAGAGTCTC 360
 QY 361 TCTGAGAGAGAGTGAATGAGTGGTGAATCTGACAAATGCTCTCTCATAGAGTGG 420
 DB 361 TCTGAGAGAGAGTGAATGAGTGGTGAATCTGACAAATGCTCTCTCATAGAGTGG 420
 QY 421 AGTGGATGCTTTTACAGATTTCTTAAACTGATGAGTGGTGGTGGTGGTGGTGGT 480
 DB 421 AGTGGATGCTTTTACAGATTTCTTAAACTGATGAGTGGTGGTGGTGGTGGTGGT 480
 QY 481 GGTGGCTGTGAAGACTTCAAGAAATGCAAGAACTCAACAAATCATCTTAAAGCAAA 540
 DB 481 GGTGGCTGTGAAGACTTCAAGAAATGCAAGAACTCAACAAATCATCTTAAAGCAAA 540
 QY 541 GSCAATCTATGAGAAATTCATTCAGATGATGCTCCCAAGAGAGTAAATGATTTTCA 600
 DB 541 GSCAATCTATGAGAAATTCATTCAGATGATGCTCCCAAGAGAGTAAATGATTTTCA 600
 QY 601 TACTAAGAAAGTAAATGCTTAAGAGATGCTCCAGCCCACTTCCACAGTTTGTACGGC 660
 DB 601 TACTAAGAAAGTAAATGCTTAAGAGATGCTCCAGCCCACTTCCACAGTTTGTACGGC 660
 QY 661 ACAAGCAGAGTGTACCACTCATGCAATGATGATGATGATGATGATGATGATGATG 720
 DB 661 ACAAGCAGAGTGTACCACTCATGCAATGATGATGATGATGATGATGATGATGATG 720
 QY 721 GACCTACTTACATTTGATAGAGAGAGACTTCAAGAGACCAACAACTTTAGAGACGATC 780
 DB 721 GACCTACTTACATTTGATAGAGAGAGACTTCAAGAGACCAACAACTTTAGAGACGATC 780
 QY 781 AGATCATTTACTTACAAATGATTCAGATGATGATGATGATGATGATGATGATGATG 840
 DB 781 AGATCATTTACTTACAAATGATTCAGATGATGATGATGATGATGATGATGATGATG 840
 QY 841 AGTAAAGATCATTTGCTCTTTTGTAGTGTATGTATCTAATAATATATATAATA 900

DB 841 AGTAAAGATCATTTGCTCTTTTGTAGTGTATGTATCTAATAATATATAATA 900
 QY 901 CTAATGTGTACTCTAATAATATAGCTTGTGTATTAAGAGAGATGATTTTCAATTT 960
 DB 901 CTAATGTGTACTCTAATAATATAGCTTGTGTATTAAGAGAGATGATTTTCAATTT 960
 QY 961 ACACCATGCAATATATTAATGTAAGAACTTTTATTTATTTATTTATTTATTTATTT 1020
 DB 961 ACACCATGCAATATATTAATGTAAGAACTTTTATTTATTTATTTATTTATTTATTT 1020
 QY 1021 ATCTATCTTCCGAAATATTTATGAAATCTATCTGATTTCTATTAATAAATTTCT 1080
 DB 1021 ATCTATCTTCCGAAATATTTATGAAATCTATCTGATTTCTATTTATTAATAAATTTCT 1080
 QY 1081 TATTTTCAATAACAGTCAAGTAAGAGAGAGCTTTTGAAGCCGAATTCAGACACCTGGC 1140
 DB 1081 TATTTTCAATAACAGTCAAGTAAGAGAGAGCTTTTGAAGCCGAATTCAGACACCTGGC 1140
 QY 1141 GCGGTACTAGTGGATCCGAGCTC 1164
 DB 1141 GCGGTACTAGTGGATCCGAGCTC 1164

RESULT 2
 AAD42498
 ID AAD42498 standard; cDNA; 1164 BP.
 XX AC AAD42498;
 XX DT 15-NOV-2002 (first entry)
 XX DE Murine regulator of G-protein signalling (RGS) protein, ml975 cDNA.
 XX KW Murine; screening; RGS; regulator of G-protein signalling; pancreatitis;
 KW inflammatory disorder; allergy; Grave's disease; arthritis; sinusitis;
 KW respiratory disorder; asthma; pneumonia; therapy; immune disorder;
 KW haematological disorder; haemopoiesis; platelet-associated disorder;
 KW thrombocytopaenia; migration; invasive disorder; leukaemia; anaemia;
 KW erythrocyte-associated disorder; hepatitis; ml975; gene; ss.
 XX OS Mus sp.
 XX FH Key Location/Qualifiers
 FT CDS 134..841
 FT /*tag= a
 FT /product= "Murine RGS protein"
 XX US6410240-B1.
 XX PD 25-JUN-2002.
 XX PF 04-FEB-2000; 2000US-00498959.
 XX PR 04-FEB-1999; 99US-00244314.
 XX PA (MILL-) MILLENIUM PHARM INC.
 XX PI Hodge MR, Yowe D;
 XX WPI; 2002-588886/63.
 XX P-PSDB; AAE25830.
 XX Screening assays for identifying agent that binds to human or mouse RGS
 XX (regulators of G-protein signalling) protein or its variant, or RGS
 XX protein encoded by homologous DNA sequences, or to host cell expressing
 XX the proteins.
 XX Claim 15; Col 55-58; 42pp; English.
 XX The invention relates to screening assays for identifying an agent that
 CC binds to: human or mouse RGS (regulators of G-protein signalling) protein
 CC or its variant, or RGS protein encoded by homologous DNA sequences; or a
 CC host cell expressing the RGS protein or its variant, or RGS protein

CC encoded by homologous DNA sequences. The invention is useful for
CC identifying an agent that binds to human or mouse RGS protein or its
CC variant, or RGS protein encoded by homologous DNA sequences, or a host
CC cell expressing the RGS protein or its variant, or RGS protein encoded by
CC homologous DNA sequences. The agents identified using the invention are
CC useful for modulating the activity of RGS proteins and thus useful for
CC treating immune and inflammatory disorders (Grave's disease, allergy,
CC arthritis), respiratory disorders (asthma, pneumonia, sinusitis),
CC haematological disorders (haematopoiesis, migration), platelet-associated
CC disorders (thrombocytopenia), invasive disorders (leukaemia),
CC erythrocyte-associated disorders (anaemia), pancreatitis, hepatitis etc.
CC The present sequence is murine RGS protein, ml975 cDNA
XX
SQ Sequence 1164 BP; 406 A; 202 C; 222 G; 334 T; 0 U; 0 Other;
Query Match 100.0%; Score 1164; DB 6; Length 1164;
Best Local Similarity 100.0%; Pred. No. 4.7e-246;
Matches 1164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGTGAAGAAATCTGAGGAAGATTCCGGATAGCGCTTTATTCAGGATGTTTCCT 60
Db 1 TTTTGTGAAGAAATCTGAGGAAGATTCCGGATAGCGCTTTATTCAGGATGTTTCCT 60
Qy 61 ATGAAATAGCATTCATCTGTGGGAGAGAGAGGACTTAAGAAATCTGACATCTGTGGTC 120
Db 61 ATGAAATAGCATTCATCTGTGGGAGAGAGAGGACTTAAGAAATCTGACATCTGTGGTC 120
Qy 121 ACTGGGACAGAAATATGATATGTCCTGCTTTCTCTCAATTAATATGTGTGAATC 180
Db 121 ACTGGGACAGAAATATGATATGTCCTGCTTTCTCTCAATTAATATGTGTGAATC 180
Qy 181 AAAGAGAGAACTTTTTCAACTTAATGCAATGCGTTCAGGGAAGAAAGAAACAGATCGA 240
Db 181 AAAGAGAGAACTTTTTCAACTTAATGCAATGCGTTCAGGGAAGAAAGAAACAGATCGA 240
Qy 241 GGCCAAATCAGACGAAAGAAAGAAATAGACTAAGTCTTCTCTACAGAGCGCTGA 300
Db 241 GGCCAAATCAGACGAAAGAAAGAAATAGACTAAGTCTTCTCTACAGAGCGCTGA 300
Qy 301 CTTCATGGAGAGACTCAGGACAGTAGATCGCCCTCTTGCCCAAGAAACAGAGCTC 360
Db 301 CTTCATGGAGAGACTCAGGACAGTAGATCGCCCTCTTGCCCAAGAAACAGAGCTC 360
Qy 361 TCCTGAAGAACAGTGAATGGCTGAATCATATTGACAAATGCTCTCATAGAGATGG 420
Db 361 TCCTGAAGAACAGTGAATGGCTGAATCATATTGACAAATGCTCTCATAGAGATGG 420
Qy 421 AGTGGATGCTTTTACCAGATTTCTTAAATCTGAATTCAGTGAGGAGAACATTTGTTG 480
Db 421 AGTGGATGCTTTTACCAGATTTCTTAAATCTGAATTCAGTGAGGAGAACATTTGTTG 480
Qy 481 GGTGCGCTGTCAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTTAAAGCAA 540
Db 481 GGTGCGCTGTCAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTTAAAGCAA 540
Qy 541 GGCATCTATCAGAAATTCATTGAGATGATGTCGCCCAAGAGGTTAAACATTTGATTCA 600
Db 541 GGCATCTATCAGAAATTCATTGAGATGATGTCGCCCAAGAGGTTAAACATTTGATTCA 600
Qy 601 TACTAAGAAATGATGTAGAGATCGCCACCCACCTCTCCACAGTTTGTATAGCGC 660
Db 601 TACTAAGAAATGATGTAGAGATCGCCACCCACCTCTCCACAGTTTGTATAGCGC 660
Qy 661 ACAAGCAGAGTGTACCAAGCTCATGGAAATGACAGTTTAAACGCTTTTGAATCTGA 720
Db 661 ACAAGCAGAGTGTACCAAGCTCATGGAAATGACAGTTTAAACGCTTTTGAATCTGA 720
Qy 721 GACCTACTTACATTTGATAGAGAGACCTCAGAGACCAACAAACCTTAGGACGATC 780
Db 721 GACCTACTTACATTTGATAGAGAGACCTCAGAGACCAACAAACCTTAGGACGATC 780
Qy 781 ACGATCATTTTACTTACATATGTTTCCAGATGTTAAAGTCAGATGTCGATTCCTGTTATG 840
Db 781 ACGATCATTTTACTTACATATGTTTCCAGATGTTAAAGTCAGATGTCGATTCCTGTTATG 840

Db 781 ACGATCATTTACTTACATATGTTTCCAGATGTTAAAGTCAGATGTTGCCATTTGGTTATG 840
Qy 841 AGTAAAGTCATTTGCTTTCTTTTGGATAGTGTATGTATATCTATAATAATAATAATA 900
Db 841 AGTAAAGTCATTTGCTTTCTTTTGGATAGTGTATGTATATCTATAATAATAATAATA 900
Qy 901 CTAATGTGTACTTCTAAATATATAGCTTGTGTATAAGAGAGATGATTTCAATTTAAAT 960
Db 901 CTAATGTGTACTTCTAAATATATAGCTTGTGTATAAGAGAGATGATTTCAATTTAAAT 960
Qy 961 ACACATGCAAAATACATATTAATGTAGAACTTTTATATATATACTAAAAATTAATCATC 1020
Db 961 ACACATGCAAAATACATATTAATGTAGAACTTTTATATATACTAAAAATTAATCATC 1020
Qy 1021 ATCTATCTTCCGAATATTTTATGAAATCTATCTGATATTTCTATCTATATAATAATCTT 1080
Db 1021 ATCTATCTTCCGAATATTTTATGAAATCTATCTGATATTTCTATCTATATAATAATCTT 1080
Qy 1081 TATTTCTACAATAACAGTCAGTAAGAGAGCTTTTGAAGCCGAATTCAGACACACTGGCG 1140
Db 1081 TATTTCTACAATAACAGTCAGTAAGAGAGCTTTTGAAGCCGAATTCAGACACACTGGCG 1140
Qy 1141 GCGGTACTAGTGGATCCGAGCTC 1164
Db 1141 GCGGTACTAGTGGATCCGAGCTC 1164
RESULT 3
ABQ99387
ID ABQ99387 standard; cDNA; 1884 BP.
XX
AC ABQ99387;
XX
DT 25-FEB-2003 (first entry)
XX
Human coding sequence SEQ ID 120.
DE
XX Human; expressed sequence tag; EST; chromosome 16;
KW haematopoietic disorder; central nervous system disease; viral infection;
KW peripheral nervous system disease; non-healing wound; infectious disease;
KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
KW fungal infection; autoimmune disorder; coagulation disorder; neutropenic;
KW anti-allergic; anti-inflammatory; immunosuppressive; neuroprotective;
KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
KW immunostimulant; cerebroprotective; gene therapy; gene; ss.
XX Homo sapiens.
OS
XX WO200259260-A2.
PN
XX 01-AUG-2002.
PD
XX 16-NOV-2001; 2001WO-US042950.
PF
XX 17-NOV-2000; 2000US-00714936.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
XX WPI; 2002-590824/63.
DR N-PSDB; ABP64801.
XX
XX New isolated polynucleotide, useful in research, diagnostic or
PT therapeutic methods, e.g. preventing or treating disorders involving
PT aberrant protein expression or biological activity.
XX
PS Claim 1; SEQ ID NO 120; 394pp; English.
XX
XX The present invention relates to novel human coding sequences (ABQ99268-
CC ABQ99608) and proteins (ABP64682-ABP65022). The sequences are useful in
CC therapeutic, diagnostic and research methods. The polynucleotides may be

used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polynucleotides are useful in diagnostics as expressed sequence tags (ESTs) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polynucleotides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral nervous system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, infectious diseases caused by viral, bacterial or fungal infection, autoimmune disorders, allergic reactions and conditions, coagulation disorders, or cancer. The polynucleotide sequences of the invention were assembled from ESTs isolated mainly by sequencing by hybridisation, and in some cases, sequences obtained from one or more public databases. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 51.8%; Score 602.6; DB 6; Length 1884;
Best Local Similarity 75.3%; Pred. No. 1.2e-122;
Matches 817; Conservative 0; Mismatches 234; Indels 34; Gaps 4;
SQ Sequence 1884 BP; 681 A; 314 C; 328 G; 561 T; 0 U; 0 Other;
1 TTTTGTAAAGAAATCTGAGGAAGATTCGGGATAGCGCTTTATTC-AGGATGTTTCC 59
25 TTTCTTTTGTAAACATCTGTGTAGAGTTGTGATCTTTTATCTACTATGATG 84
60 TATGAAATAGCATTCATCTGTGGGAGAGAGAGACTAAGAAATCTGACATCTGGT 119
85 TATGGAATAGTATTAATAATGAACATAGGGAAGATGTAATAAATTAGACATCTCTCAT 144
120 CACTGGGACAGATATGATGTCACCTGTTTCTTCTCTCAATTAATATGTCGAAT 179
145 T--TTAGAGAGAGATGGAACACATCTGTTTCTTCTTCTCAATTAATATGTCGAAT 202
180 CAAAAGAGAAATCTTTTTCACAACTAATGATGCTGAGGAAAGAGAAACAGCATCG 239
203 CAAAAGAGAAATCTTTTTCACAACTAATGATGCTGAGGAAAGAGAAACAGCAAG 262
240 AGGCCAAATCAGACGGAAGAAAGAAAGATAGACTAAGTCTTCTCTACAGAGGCTG 299
263 AAGCCAAATCAGAGCTAAGGAAAGAAAGAAATAGACTAAGTCTTCTTGTGAGAAACCTG 322
300 ACTTCCATCGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAACAGAGTCT 359
323 AGTTTCATGAGACACCCGCTCCAGTAGATCTGGGCACTTGGCCAAAGAAACAGAGTCT 382
360 CTCCTGAAGAGACAGTGAATGGGCTGATCATTTGACAAATTCCTCTCATAGAGATG 419
383 CCCCTGAAGAGAGCAGTGAATGGGCTGATCATTTGACAAATTCCTTCCCATAGAGATG 442
420 GAGTGGATGCTTTTACCAGATTTCTTAAATCTGAATTCAGTGAGGAGAAACATTCGAATTT 479
443 GACTAGAGGCTTTTACCAGATTTCTTAAATCTGAATTCAGTGAGGAGAAATATTCGAATTT 502
480 GGGTCCCTGTGAAGACTTCAAGAAATCAGAGAACTCAACAAATCATCTCTAAAGCAA 539
503 GGATAGCCTGTGAGATTTCAAGAAAGCAAGGAGACCTCAACAAATTCACCTTAAAGCAA 562
540 AGGCAATCTATGAGAAATCTATCAGATGATGCCCCCAAGAGGTTAAACATTCATTTTC 599
563 AAGCAATATGAGAAATTTATACAGATGATGCCCCCAAGAGGTTAAACATTCATTTTC 622
600 ATACTAAAGAGTAAATCTTAAAGAGCATCGCCAGCCACCTCTCCACAGTTTTCATACGG 659
623 ACACAAAGAGTCAATACAAACAGCATCACTCAACCTACCTCCACAGTTTTCATGCTG 682

QY 660 CACAAAGCAGAGTGACACAGCTCATGGAACATGACAGTTATAACGCTTTTGAATCTG 719
Db 683 CACAAAGCAGAGTGATCATGCTCATGGAACAGAGAGTTATACAGCTTTTCTGAATCTG 742
QY 720 AGACCTACTTACATTTGATAGAGGAGACCTCAGAGACCAACCAACCTTAGGAGACGAT 779
Db 743 ACATCTATTATGACTTGATGAGGAGACCTCAGAGACCAACCAACCTTAGGAGACGAT 802
QY 780 CAGCATCAATTTACTTTACATGATTTCCAGAGTGTAAAGTCAAGTTCCTCATTTCCATTTAT 839
Db 803 CAGGCTCATTTTACCTGCAATGAATCCCAAGATGTACAATCAGATGTCCTCATTTGCTTAT 862
QY 840 GAGTAAAGTCAATTTGCTTCTTTTGTAGTGTATGTATATCTATAATATACTATAAT 899
Db 863 AAGAAATTTGATTTTGTCTCATTTTATGACAACTTATACATC----- 906
QY 900 ACTAATGTCTACTTCTTAAATATAGCTTGTGTATAGAGAGATGATTTCAATTT----- 954
Db 907 -----TGCTTCTACATATCGCATGTTTATGTTTAAAGATTGGTCCCATCTTAA 957
QY 955 -TAAATACACCATGCAATATCATATTAATGTAAAGACTTTTATATATATATATAATA 1013
Db 958 CTGAATATGTCATGTGAATTTATTTTAAATGTAAAAACAAACTTTCTGCTAACAAA 1017
QY 1014 ATTCACTCATCTATCTTCCGAAATATTTTATGAAATCTATCTGATATCTTATCTAATA 1073
Db 1018 ATACATACAGTATCTGCCAGTATATCTGTAAGACCTTCTATTGATGTCATTCATTA 1077
QY 1074 AATTC 1078
Db 1078 TAATC 1082
RESULT 4
AAS18339
ID AAS18339 standard; DNA; 1840 BP.
XX AAS18339;
AC AAS18339;
XX
DT 12-MAR-2002 (first entry)
XX
DE 5'-RACE clone DNA used to generate full length human RGS18 cDNA.
XX
KW Human; regulator of G protein signalling; RGS18; arterial thrombosis;
KW platelet activation dysfunction; myocardial infarction; stroke;
KW coronary artery disease; cerebrovascular disease; unstable angina;
KW deep vein thrombosis; systemic thromboembolism; anti-coagulant;
KW invasive cardiac procedure; 5'-RACE; ds.
XX
OS Homo sapiens.
XX
PN WO200183514-A2.
XX
PD 08-NOV-2001.
XX
PF 26-APR-2001; 2001WO-US013540.
XX
PR 28-APR-2000; 2000US-0200786P.
PR 02-AUG-2000; 2000GB-00018833.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
XX Murray D., Gagnon AW;
PI MPI; 2002-055453/07.
XX
XX Isolated regulator of G protein signaling polypeptide, useful for
PT prevention/treatment of platelet activation dysfunction, such as arterial
PT thrombosis, myocardial infarction, coronary artery disease and stroke.
XX
PS Claim 1; Page 116-117; 127pp; English.
XX

The present invention relates to the isolation of polynucleotide sequences that encode a novel regulator of G protein signalling (RGS) polypeptide, RGS18, from human platelets. The invention also provides nucleotide primers and probes specific for an RGS18 nucleic acid. The sequences of the invention are useful for the manufacture of a medicament for the prevention or treatment of a platelet activation dysfunction, such as arterial thrombosis, myocardial infarction, coronary artery disease, stroke, cerebrovascular disease, unstable angina, deep vein thrombosis, systemic thromboembolism, and in invasive cardiac procedures for anti-coagulant purposes. The sequences of the invention can also be used for the detection of RGS18 nucleic acids and RGS18 polypeptides. The present sequence represents 5'-RACE clone DNA used to generate the full length human RGS18 cDNA

Sequence 1840 BP; 668 A; 309 C; 328 G; 535 T; 0 U; 0 Other;

Query Match 51.5%; Score 599.6; DB 6; Length 1840;
Best Local Similarity 75.2%; Pred. No. 5.2e-124; Indels 34; Gaps 4;
Matches 814; Conservative 0; Mismatches 22;

QY 4 TTGTAAGAAAATCTGAGGAAAGATTCGGGATAGCGCTTTATTC-AGGATGTTTTCCTAT 62
DB 34 TTTTGTGTAACATTTACTGTGAAGTGTGTGATACTTTTATTCTACTATGATATGAT 93
QY 63 GAATAGCAATTCATCTGTGGAGAGAGAGACTAAGGAATCTGACATCTGTTGGTCAC 122
DB 94 GGAATAGTATTAATAAATGAATAGGAGAGATGTAATAAATTAGACATCTCTTCATT-- 151
QY 123 TGGGACAGAAATGGAATGTCATGCTGTTTCTCTCTCAATTAATAATGTTGTAATCAA 182
DB 152 TTAGAGAGAGTGGAAACATCTGTTTCTTCTCAATTAATAATGTTGTAATCAA 211
QY 183 AAGAGAAATCTTTTCAAACTAATGTCATGCGGTGAGGAAAGAGAAACAGATCTGAGG 242
DB 212 AAGAAAAATCTTTTCAAGTTAATACATGTTTTCAGGAAAAAGAGAAACAGCAAGAG 271
QY 243 CCAGAAATCAGAGCGAAGAAAAAGGATACAGTAAGTCTCTCTCAGAGGCTGACT 302
DB 272 CCAGAAATCAGAGCTAAGGAAAAAGAAATAGACATGATGCTCTTCTGTCAGAACTGAGT 331
QY 303 TCCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAAGAAACAGATCTCTC 362
DB 332 TCCATGAGAGACACCGCTCCAGTAGATCTGGCCACTTGGCCAAAAGAAACAGATCTCCC 391
QY 363 CTGAAGAGCAGTGAATGGGCTGATCATTTGACAAATGCTCTCTCATAGAGATGAG 422
DB 392 CTGAAGAGCAGTGAATGGGCTGATCATTTGACAAATGCTCTTCCCATAGAGATGAGC 451
QY 423 TGGATGCTTTTACCAGATTTCTTAAACTGAAATTCAGTGAAGAGAAACATTTGGG 482
DB 452 TAGAGGCTTTTACCAGATTTCTTAAACTGAAATTCAGTGAAGAGAAATATTGAATTTGGA 511
QY 483 TCGCCTGTGAGAGACTTCAAGAAATGCAAGGAACTCAACAAATCATCTTAAAGCAAGG 542
DB 512 TAGCCTGTGAGAGATTTCAAGAAAAAGCAAGGACCTCAACAAATTCACCTTAAGCAAGG 571
QY 543 CAATCTATGAGAAATTCATTCAGATGATGCCCCAAAAGAGTTAAACATTCATTTTCATA 602
DB 572 CAATATATGAGAAATTTATACAGACTGATGCCCAAGAGGTTAACTCGATTTTCACA 631
QY 603 CTAAGAAGATTAATGCTAAGAGCATTCGCCAGCCACCTCTCCACAGTTTTCATACGGCAC 662
DB 632 CAAAAGAAAGTCATTAACAACAGCATCACTCAACCTACCCCTCCACAGTTTTCATGCTGCAC 691
QY 663 AAAGCAGAGTGTACAGCTCATGGAACATGACAGTTATAAAGCTTTTGGAAATCTCAGA 722
DB 692 AAAGCAGAGTGTATCAGCTCATGGAACAGAGTTATACACGTTTCTGAAATCTGACA 751
QY 723 CCTACTTACATTTGATAGAGGAGACCTCTCAGAGACCAACAAACCTTAGGAGAGCATCAC 782
DB 752 TCTATTTAGACTTGTAGGAGAGAGACCTCAGAGACCAACAAATCTTAGGAGAGCATCAC 811
QY 783 GATCATTTACTTACAAATGATTTCCAAAGATGTAAAGTCAGATGTTGCCATTTGGTTATGAG 842

DB 812 GCTCAATTTACCTGCAATGAATCCAGATGTACAAATCAGATGTGCCATTTGGTTATAAA 871
QY 843 TAAAGTCAATTTGCTCTTCTTTTCAAGTAGTGTATGCTGTATATCTAAATATATACTAAT 902
DB 872 GAAAAATGATTTTGGCTCAATTTTATGACAACTTATACATC----- 912
QY 903 AATGTCTACTTCTTAAATAATAGCTTTGTGTATAGAGAGAGATGATTTTCATTTT-----TA 956
DB 913 -----TGCTTCTAACATATGCAATGTTTATGTTAAGATTTGGTCCCATCTTAAACTG 966
QY 957 AATACACCATGCAATATACATATTAATGTAAGAACTTTTATATATATATACTAAATAATT 1016
DB 967 AATATGTCTGTAATGAAATTTTAAAAATGTAAGAACTTTTCTGCTACAAAAATA 1026
QY 1017 CATCATCTATCTTCCGAAATATTTTATGAAATCTATCTGATATCTATCTATTAATAAAT 1076
DB 1027 CATACAGTATCTGCCAGTATATCTGTAAGAACTTCTATTTGATGTCATTCATTTATTA 1086
QY 1077 TC 1078
DB 1087 TC 1088

RESULT 5
AAS18340
ID AAS18340 standard; cDNA; 2144 BP.
XX
AC AAS18340;
XX
DT 12-MAR-2002 (first entry)
XX
DE Full length cDNA encoding human RGS18.
XX
KW Human; regulator of G protein signalling; RGS18; arterial thrombosis; platelet activation dysfunction; myocardial infarction; stroke;
KW coronary artery disease; cerebrovascular disease; unstable angina;
KW deep vein thrombosis; systemic thromboembolism; anti-coagulant;
KW invasive cardiac procedure; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 163..870
FT /*tag= a
FT /product= "RGS18 polypeptide"
XX
PN WO200183514-A2.
XX
PD 08-NOV-2001.
XX
PF 26-APR-2001; 2001WO-US013540.
XX
PR 28-APR-2000; 2000US-0200786P.
PR 02-AUG-2000; 2000GB-00018833.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
PI Murray DL, Gagnon AW;
XX
DR WPI; 2002-055453/07.
DR P-PSDB; AAU10749.
XX
PT Isolated regulator of G protein signalling polypeptide, useful for prevention/treatment of platelet activation dysfunction, such as arterial thrombosis, myocardial infarction, coronary artery disease and stroke.
PS Claim 1; Fig 1; 127pp; English.
XX
CC The present invention relates to the isolation of polynucleotide sequences, that encode a novel regulator of G protein signalling (RGS) polypeptide, RGS18, from human platelets. The invention also provides nucleotide primers and probes specific for an RGS18 nucleic acid. The

sequences of the invention are useful for the manufacture of a medicament for the prevention or treatment of a platelet activation dysfunction, such as arterial thrombosis, myocardial infarction, coronary artery disease, stroke, cerebrovascular disease, unstable angina, deep vein thrombosis, systemic thromboembolism, and in invasive cardiac procedures for anti-coagulant purposes. The sequences of the invention can also be used for the detection of RGS18 nucleic acids and RGS18 polypeptides. The present sequence represents the full length cDNA sequence encoding RGS18 from human platelets.

Sequence 2144 BP; 784 A; 340 C; 365 G; 655 T; 0 U; 0 Other;

Query Match	51.5%;	Score 599.6;	DB 6;	Length 2144;
Best Local Similarity	75.2%;	Pred. No. 5.4e-122;		
Matches 814;	Conservative	0;	Mismatches 234;	Indels 34;
				Gaps 4

Qy	4	TTGTAAGAAAAATCTGAGGAAAGATTGGGATACGGCTTTATTTC-AGGATGTTTTCCTAT	62
Db	34	TTTTTTGTAAACATTTACTGTAAAGAGTTGTGTAACTTTTATTCTACTATGTATATGTAT	93
Qy	63	GAATAGCAATTCATCTGTGGGAGAGAGAAGGACTTAAGGAAATCTGACATCTGTGTGTCAC	122
Db	94	GGAA TAGTATTAAATAAATGAAC TAGGAAGGATGTAATAATTAGACATCTCTTCATT--	151
Qy	123	TGGGACAGNATATGATATGTCAC TGGTTTTCTCTCTCAATTAATATGTGTGATCAA	182
Db	152	TTAGAGAGAGAAGATGGAACAACATTTGCTTTTCTCAAAATAATATGTGTGAATCAA	211
Qy	183	AAGAGAAAACTTTTTTTCAAACTAATGTCATGGGTGAGGAAAGAGAAAACAAGCATCGGG	242
Db	212	AAGAAAAAATTTTTTCAAGTTAATACATGTTTCAGGAAAAGAGAAAAACAAGCAAGAAG	271
Qy	243	CCAAATCAGACGCGAAGAAAAAGGAATAGACTTCTCTCTCTACAGAGCCCTGACT	302
Db	272	CCAAATCAGAGCTAAGGAAAAAGAAATAGACTTAAGTCTTCTGTGCGAGAAACCTGAGT	331
Qy	303	TCCATGGAGAGACTCAAGCCAGTAGATCTGCCCTCTTTGGCCAAAGAGAAAACAAGATCTCTC	362
Db	332	TTTCATGAAGACACCCGCTCCAGTAGACTTGGGCACCTTGGCCAAAGAGAAAACAAGATCTCC	391
Qy	363	CTGAGAGACGAGTGAATGGGCTGCAATCTTGACAAATTGCTCTCTCATAGAGATGGAG	422
Db	392	CTGAAGAGCGAGTGAATGGGGTGAATCATTTGCAAACTGCTTTCCCATAGAGATGGAC	451
Qy	423	TGGATGCTTTTACCAGATTCTTTAAAAC TGAATTCAGTGAGGAGAACATTTGAATTTGGG	482
Db	452	TAGAGGCTTTTACCAGATTCTTTAAAAC TGAATTCAGTGAGGAGAAAATATTGAATTTTGA	511
Qy	483	TGCGCTGTGAGACATTCAGAAAAATGCAAGAACCTCAACAAATCATCTTAAAGCAAGG	542
Db	512	TAGCCTGTGAGATTTCAAGAAAGCAAGGACCTCAACAAATTCACCTTAAGCAANAAG	571
Qy	543	CAATCTATGAGAAATTCATTCAGAAATGATGCCCCAAAGAGGTTAACTGATTTTCATA	602
Db	572	CAATATATGAGAAATTTATACAGACTGATGCCCCAAAGAGGTTAACTCGATTTTTCACA	631
Qy	603	CTAAGAAGATTAATTCCTAAGAGCATCGCCAGGCCACTCTCCACAGTTTGTGATCGGCAC	662
Db	632	CAAAAGAGTCATTTACAAACAAGCATCACTCAACCTACCTCCACAGTTTGTGCTGCAC	691
Qy	663	AAAGCAGAGTGTAACAGCTCATGGAACAATGACAGTTTATAACGCTTTTGAATATCTGAG	722
Db	692	AAAGCAGAGTGATCAGCTCATGGAACAAGACAGTTATACACGTTTCTTGAATATCTGAC	751
Qy	723	CCCTACTCATTTGATAGAAGGAAGACTCAGAGACCACCAAAACCTTAGGAGACGATCAC	782
Db	752	TCTATTTAGACTTTGATGAAGAGAGACCTCAGAGACCACCAATCTTAGGAGACGATCAC	811
Qy	783	GATCATTTTACTTACAAATGATTTCCAAGATGTAAAGTCAGATGTGGCATTTGGTTATGAG	842
Db	812	GTCTAATTTACCTGCAATGAATTCCAAGATGTACAAATCAGATGTGGCATTTGGTTATAAA	871
Qy	843	TAAGAAGTCATTTGCTCTTTTGTAGTGTATGTATATCTAAAAATATATACTAATACT	902

Query Match	51.2%;	Score 596;	DB 6;	Length 2217;	
Best Local Similarity	75.8%;	Pred. No. 3.4e-121;			
Matches 791;	Conservative 0;	Mismatches 220;	Indels 33;	Gaps 3;	
QY	41	TTTATTTCAGGATGTTTCTCTATGAATAGCAATTCATCTGTGGGAGAGAGGACTAAGG	100		
DB	69	TTATTCTACTATGATATGATGTAATAGTATTAATAATGAACCTAGGAGGAGTGAAT	128		
QY	101	AAATCTGACATCTGTTGGTCACTGGGACAGATATGATATGTCACCTGGTTTCTTCTCT	160		
DB	129	AAATTAGACATCTCTTCAT--TTTATGAGAGAGATGGAACAACATTCCTTTCTTCT	186		
QY	161	CAATTAATATGTTGTAATCAAAAGAGAAACTTTTTTCAAACTAATGCGATGGTCAGGG	220		
DB	187	CAATTAATATGTTGTAATCAAAAGAGAAACTTTTTTCAAGTTAATACATGTTTCAGGA	246		
QY	221	AAAGAGAAACAGCATCGAGCCCAATTCAGAGCGAAGAAAGAAAGGATAGACTAAGT	280		
DB	247	AAAGAGAAACAGCAAGAAAGAGCCCAATTCAGAGCTAAGGAAAGAAAGAAATAGACTAAGT	306		
QY	281	CTTCTCTACAGAGGCTGACTTCCATGGAGAGACTCAAGCCAGTAGATCTGCCCTCTTG	340		
DB	307	CTTCTTGTGCGAAGAACCTGAGTTTCATGAGAGACCCGCTCCAGTAGATCTGGGCACTTG	366		
QY	341	GCCAAAGAAACAGAGTCTCTCTGAAAGAGCAGTGAATGGGCTGAAATCAATTTGACAAA	400		
DB	367	GCCAAAGAAACAGAGTCTCTCTGAAAGAGCAGTGAATGGGCTGAAATCAATTTGACAAA	426		
QY	401	TTGCTCTCATGAGATGGAGTGTGCTTTTACCAGATTTCTTAAACTGAATTCAGT	460		
DB	427	CTGCTTTCCCATGAGATGGACTAGAGGGCTTTTACCAGATTTCTTAAACTGAATTCAGT	486		
QY	461	GAGGAGAACATGAAATTTGGGTGCGCTGTGAGAGACTTCAAGAAATCAAGGAACTTCAA	520		
DB	487	GAAGAAATATGAAATTTGGATGAGCTGTGAGAGATTTCAAGAAAGCAAGGACCTCAA	546		
QY	521	CAAAATCATCTAAAGCAAGGCAATCTATGAGAAATTCATTCAGATGATGCCCCAAA	580		
DB	547	CAAAATTCAGCTTAAAGCAAGGCAATATATGAGAAATTTATACAGACTGATGCCCCAAA	606		
QY	581	GAGGTTAACTGATTTTTCATCAAGAAAGTAAATGCTAAGAGCATCGCCAGCCCACT	640		
DB	607	GAGGTTAACTGATTTTTCACAAAGAGAGTCAATTAACAAAGCATCACTCAACCTACC	666		
QY	641	CTCCACAGTTTGTATACGGCAACAAAGCAGAGTGTACAGCTCATGGAACATGACAGTTAT	700		
DB	667	CTCCACAGTTTGTATGCTGCAACAAAGCAGAGTGTATCAGCTCATGGAACAAAGACAGTTAT	726		
QY	701	AAACGCTTTTGAATCTGAGACCTACTTACATTTGTATAGAGAGAGCACTCAGAGACCA	760		
DB	727	ACAGCTTTTCTGAATCTGACATCTATTATAGACTTTGATGGAAGAGAGCACTCAGAGACCA	786		
QY	761	ACAAACCTTAGAGAGCATCAGATCAATTTACTTACAAATGATTTCCAAAGATGTAAGTCA	820		
DB	787	ACAACTCTTAGAGAGCATCAGCTCAATTTACTGCAATGAATTTCCAAAGATGTAAGTCA	846		
QY	821	GATGTTGCCATTTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	880		
DB	847	GATGTTGCCATTTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	906		
QY	881	ATCTAAATATATATACTAATAATGATGATGATGATGATGATGATGATGATGATGAT	940		
DB	907	ATC-----TGCTTCTAATATATGATGATGATGATGATGATGATGATGATGATGAT	941		
QY	941	GATGATTTCAATTT-----TAAATACACCATGCAATACATATTAATGTAAGACTT	994		
DB	942	TTTGCTCCATCTTTAACTGAATATGTCATGTGAAATTTATTTTAAATGATGTAAGAAAC	1001		
QY	995	TTTATATATATATAAAT	1054		
DB	1002	AAACTTTCTGCTAACAAATATACATAGATATCTGCCAGTATATCTGTAAACCTTCTA	1061		
QY	1055	TGATATTTCTTATTAATAAATTC	1078		
Db	1062	TTTGATGTCATTCCTCCATTTATAATC	1085		
RESULT 8					
ABQ98617					
ID	ABQ98617	standard; DNA; 848 BP.			
XX	ABQ98617;				
AC	XX	04-NOV-2002 (first entry)			
DT	XX	Human ORF424 coding sequence.			
DE	XX	Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnary;			
KW	XX	Antiinflammatory; gene therapy; human; ORFX; atherogenic; platelet;			
KW	XX	human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;			
KW	XX	cancer; cardiovascular disease; allergy; autoimmune disease;			
KW	XX	wound healing; blood coagulation disorder; inflammatory disorder; ds.			
OS	XX	Homo sapiens.			
XX	XX	US2002082206-A1.			
PN	XX	27-JUN-2002.			
PD	XX	30-MAY-2001; 2001US-00867550.			
XX	XX	30-MAY-2000; 2000US-0208427P.			
PR	XX	(LEAC/) LEACH M D.			
XX	XX	(MEHR/) MEHRABAN F.			
PA	XX	(CONL/) CONLEY P B.			
PA	XX	(TOPE/) TOPPER J N.			
PA	XX	(LAWD/) LAW D.			
XX	XX	Leach MD, Mehraban F, Conley PB, Topper JN, Law D;			
PI	XX	WPI; 2002-626554/67.			
DR	XX	P-PSDB; ABP64054.			
XX	XX	New polypeptide designated ORFX are present in human atherogenic cells			
PT	XX	and are useful to prevent and treat ORFX-associated disorders including			
PT	XX	cancer, allergy, wound healing or autoimmune, cardiovascular or			
PT	XX	inflammatory disease.			
XX	XX	Claim 2; SEQ ID NO 847; 78pp; English.			
PS	XX	The present invention relates to novel human ORFX polypeptides and their			
CC	XX	coding sequences (ABP63631-ABP64681 and ABQ98194-ABQ99267). The sequences			
CC	XX	were discovered in human atherogenic cells, in particular in platelets			
CC	XX	and human umbilical vein endothelial cells (HUVEC) and are expressed in			
CC	XX	many other tissues as well. Atherogenic cells are cells which have the			
CC	XX	potential to develop atherosclerotic plaques. The ORFX polypeptides and			
CC	XX	nucleic acids are useful for treating or preventing a pathological			
CC	XX	condition associated with an ORFX-associated disorder, e.g. cancer,			
CC	XX	cardiovascular disease, allergy, autoimmune disease, wound healing, blood			
CC	XX	coagulation disorders or inflammatory disorders. Note: The sequence data			
CC	XX	for this patent did not form part of the printed specification, but was			
CC	XX	obtained in electronic format directly from the USPTO web site at			
CC	XX	seqdata.uspto.gov/sequence.html?DocID=20020082206			
XX	XX	Sequence 848 BP; 316 A; 149 C; 159 G; 223 T; 0 U; 1 Other;			
Query Match		48.2%;	Score 560.6;	DB 6;	Length 848;
Best Local Similarity		82.0%;	Pred. No. 1.6e-113;		
Matches 670;		Conservative 0;	Mismatches 144;	Indels 3;	Gaps 2;
QY	1	TTTTTTGTAAGAAAACTCAGGAAAGATTCCGGATAGCGCTTTATTC-AGGATGTTTCC	59		
DB	34	TTCTTTTGTGTAACATTAATTAAGAGTTGTAAGAGTTTCTTATCTTCTTCTTATGATG	93		
QY	60	TATGAATAGCATTCATCTGTGGGAGAGAGGACTAAGGAATCTGACATCTCTGGT	119		

Db 94 TATGGATAGTATTAATAAATGAAGTGGAGGATGTAATAAATAGACATCTCTCAT 153
Qy 120 CACTGGACAGATATGATATGCTACTGCTGCTTCTCTCTCAATTAATAATGCTGTAAT 179
Db 154 T--TTAGAGAGATGGAACACACATGCTTTTCTCTCAATAAATATGCTGTAAT 211
Qy 180 CAAAGAGAAACCTTTTCAAACTAATATGATGGTTCAGGGAAGAAAGAAACAGATCG 239
Db 212 CAAAGAGAAACCTTTTCAAGTAAATACATGCTTTCAGGAAAGAAAGAAACAGCAAG 271
Qy 240 AGGCAAAATCAGAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 299
Db 272 AAGCCAAATCAGAGCTTAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGCTG 331
Qy 300 ACTTCCATGGAGAGACTCAAGCCAGTAGATGCGCTCTTGGCCAAAGAAACAGAGTCT 359
Db 332 AGTTTCATGAAGACACCGCTCCAGTAGATGCTGGGCACTTGGCCAAAGAAACAGAGTCT 391
Qy 360 CTCCTGAAGAGCAGTGAATGGCTGAATCATTTGACAAATGCTCTCTCATAGATG 419
Db 392 CCCCTGAAGAGCAGTGAATGGCTGAATCATTTGACAAATGCTCTCTCATAGATG 451
Qy 420 GAGTGGATGCTTTTACAGATTTCTTAAACTGAATTCAGTGGAGGAAACATTTGAAATTT 479
Db 452 GACTAGAGGCTTTTACAGATTTCTTAAACTGAATTCAGTGGAGGAAATTTGAAATTT 511
Qy 480 GGGTGGCTGGAAGACTTCAAGAAATGCAAGAACTTCAACAAATCATCTTAAAGCAA 539
Db 512 GGATAGCCTGTGAAGATTTCAAGAAAGCAAGGACCTCAACAAATCACCTTTAAAGCAA 571
Qy 540 AGGCAATCTAGAGAAATTCATTCAGATGATGATGCCCCCAAGAGGTTAAACATTTTC 599
Db 572 AAGCAATATAGAGAAATTTAATAGACTGATGATGCCCCCAAGAGGTTAACTGATTTTC 631
Qy 600 ATACTAAGAGAGTAAATGCTAAGAGATGCGCCAGCCCACTCTCCAGTTTGTATACGG 659
Db 632 ACACAAAGAGTCAATACAAACAGCATCACTCAACCTACCTCCACAGTTTGTATCGT 691
Qy 660 CACAAGCAGAGTGTACAGCTCTGAGATGATGATGATGATGATGATGATGATGATG 719
Db 692 CACAAGCAGAGTGTATCAGCTCTGAGATGATGATGATGATGATGATGATGATG 751
Qy 720 AGACTACTTACTATTGATAGAGAGACCTCAGAGACCAACAAACCTTAGGAGAGCAT 779
Db 752 ACATCTATTAGACTTGTATGAGAGAGACCTCAGAGACCAACAAACCTTAGGAGAGCAT 811
Qy 780 CAGCATATTTACTTACATGATTTTCCAGATGATAA 816
Db 812 CACGCTCATTTACCTGCAATGAAATCCAGATGTACA 848

RESULT 9

AAS18331
ID AAS18331 standard; cDNA; 1486 BP.

AC AAS18331;

XX 12-MAR-2002 (first entry)

DE cDNA from a human thyroid library encoding C-terminal region of RGS18.

XX Human; regulator of G protein signalling; RGS18; arterial thrombosis;
KW platelet activation dysfunction; myocardial infarction; stroke;
KW coronary artery disease; cerebrovascular disease; unstable angina;
KW deep vein thrombosis; systemic thromboembolism; anti-coagulant;
KW invasive cardiac procedure; thyroid; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

PH 3..212

FT CDS /*tag= a

FT /partial
FT /product= "Carboxy-terminal region of RGS18"
FT /note= "This sequence lacks a start codon"
PN WO200183514-A2.
XX 08-NOV-2001.
PD
XX 26-APR-2001; 2001WO-US013540.
PF
XX 28-APR-2000; 2000US-0200786P.
XX 02-AUG-2000; 2000GB-00018833.
PR
XX (AVET) AVENTIS PHARM PROD INC.

XX Murray DL, Gagnon AW;

XX WPI; 2002-055453/07.

DR P-PSDB; AAU10748.

XX Isolated regulator of G protein signaling polypeptide, useful for
PT prevention/treatment of platelet activation dysfunction, such as arterial
PT thrombosis, myocardial infarction, coronary artery disease and stroke.

XX Example 2; Page 113-114; 127pp; English.

XX The present invention relates to the isolation of polynucleotide
CC sequences, that encode a novel regulator of G protein signalling (RGS)
CC polypeptide, RGS18, from human platelets. The invention also provides
CC nucleotide primers and probes specific for an RGS18 nucleic acid. The
CC sequences of the invention are useful for the manufacture of a medicament
CC for the prevention or treatment of a platelet activation dysfunction,
CC such as arterial thrombosis, myocardial infarction, coronary artery
CC disease, stroke, cerebrovascular disease, unstable angina, deep vein
CC thrombosis, systemic thromboembolism, and in invasive cardiac procedures
CC for anti-coagulant purposes. The sequences of the invention can also be
CC used for the detection of RGS18 nucleic acids and RGS18 polypeptides. The
CC present sequence represents a cDNA sequence from an incyte clone derived
CC from a human thyroid library. The sequence is used to isolate the full
CC length cDNA encoding RGS18 from human platelets

XX Sequence 1486 BP; 529 A; 235 C; 240 G; 482 T; 0 U; 0 Other;

Qy Query Match 16.5%; Score 192.2; DB 6; Length 1486;

Db Best Local Similarity 68.4%; Pred. No. 1.6e-32;

Qy Matches 311; Conservative 0; Mismatches 113; Indels 31; Gaps 2;

Qy 630 CCAGGCCACTCTCCACAGTTTGTACGGCAAGCAGAGTGACCAAGTCTCATGGAAC 689

Db 1 CTCACCTACCTCCACAGTTTGTACGGCAAGCAGAGTGATCATGGAAC 60

Qy 690 ATGACAGTTATAAAGCGCTTTTGAATCTGAGACCTACTTACATTTGTAGAGGAAGAC 749

Db 61 AAGACAGTTATACAGCTTTTCTGAAATCTGACATCTATTAGACTTGTAGGAAGAC 120

Qy 750 CTCAGAGCAACAAACCTTAGGAGAGCATCAGCATTTTACTTACATGATTTCCAG 809

Db 121 CTCAGAGCAACAAATCTTAGGAGAGCATCAGCTCATTTACCTCAATGAATTCAG 180

Qy 810 ATCTAAGTCAGATGTTGCAATTTGCTATGATGATAAAGTCATTTGCTTTTGTATG 869

Db 181 ATGTAACATCAGATGTTGCAATTTGCTATGATAAAGTAATTTGCTCATTTTATGA 240

Qy 870 TGTATGTTATATCTAAATATATATACTAATAATGTTGCTTCTTAAATATAGTTGT 929

Db 241 CAAACTTATACATC-----TGCTTCTTAAACATATCGCATGT 275

Qy 930 GTATAAGAGAGATGATTTTCATTTT-----TAAATACACCATGCAATATATAA 983

Db 276 TTATGTTAGATTTGTTCCCATCTTAACTGAAATATGTCATGGAATATTTTAA 335

Qy 984 TGTAAAGACCTTTTATATATATATATACTAAATATATCATCTATCTTCCGAAATATTTAT 1043

Db 336 AATGTAACAACTTCTGCTAACAAATACATACAGTATCTGCCAGTATATCTGT 395
 QY 1044 GAAATCTATCTGATATCTCTATCTTAATAATC 1078
 Db 396 AAACCTTCTATTTGATGTCATCTCCATTATAATC 430

RESULT 10
 AAS18334
 ID AAS18334 standard; cDNA; 241 BP.
 AC AAS18334;
 DT 12-MAR-2002 (first entry)
 DE cDNA encoding partial human platelet RGS domain.
 XX Human; regulator of G protein signalling; RGS18; arterial thrombosis;
 KW platelet activation dysfunction; myocardial infarction; stroke;
 KW coronary artery disease; cerebrovascular disease; unstable angina;
 KW deep vein thrombosis; systemic thromboembolism; anti-coagulant;
 KW invasive cardiac procedure; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 CDS 1..240
 FT /*tag= a
 FT /partial
 FT /product= "Partial RGS domain"
 FT /note= "This sequence encodes for residues 2-81 of
 AAU10747 and lacks both start and stop codons"
 XX
 XX WO200183514-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 26-APR-2001; 2001WO-US013540.
 XX
 PR 28-APR-2000; 2000US-0200786P.
 PR 02-AUG-2000; 2000GB-00018833.
 XX
 XX (AVET) AVENTIS PHARM PROD INC.
 XX
 XX Murray DL, Gagnon AW;
 PI WPI; 2002-055453/07.
 DR P-PSDB; AAU10747.
 XX
 XX Isolated regulator of G protein signaling polypeptide, useful for
 PT prevention/treatment of platelet activation dysfunction, such as arterial
 PT thrombosis, myocardial infarction, coronary artery disease and stroke.
 XX
 PS Claim 1; Page 115; 127pp; English.
 XX
 XX The present invention relates to the isolation of polynucleotide
 CC sequences, that encode a novel regulator of G protein signalling (RGS)
 CC polypeptide, RGS18, from human platelets. The invention also provides
 CC nucleotide primers and probes specific for an RGS18 nucleic acid. The
 CC sequences of the invention are useful for the manufacture of a medicament
 CC for the prevention or treatment of a platelet activation dysfunction,
 CC such as arterial thrombosis, myocardial infarction, coronary artery
 CC disease, stroke, cerebrovascular disease, unstable angina, deep vein
 CC thrombosis, systemic thromboembolism, and in invasive cardiac procedures
 CC for anti-coagulant purposes. The sequences of the invention can also be
 CC used for the detection of RGS18 nucleic acids and RGS18 polypeptides. The
 CC present cDNA sequence encodes for a partial human platelet RGS domain
 XX
 SQ Sequence 241 BP; 92 A; 52 C; 44 G; 53 T; 0 U; 0 Other;
 Query March 15.3%; Score 177.6; DB 6; Length 241;
 Best Local Similarity 83.8%; Pred. NO. 1.7e-29;
 Matches 201; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 461 GAGGAGAACATTGAATTTTGGTGCCTGTGAAGACTTCAAGAAATGCAAGAACTCAA 520
 Db 1 GAGGAAATCTGAGTTCTGGATAGCTGTGAAGATTTCAAGAAAGCAAGGACCTCAA 60
 QY 521 CAAATCATCTTAAAGCAAGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCCAA 580
 Db 61 CAAATTCACCTTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCCCAAAA 120
 QY 581 GAGGTTAATCATTTGATTTTCATATAAGAAATTAATTCCTTAAGAGATCGCCAGCCACT 640
 Db 121 GAGGTTAATCATTTGATTTTCACACAAAAGAGTCATTACAAAAGAGCATCACTCAACCTACC 180
 QY 641 CTCCACAGTTTGTATACGCGCAAAAGCAGAGTGTTACAGCTCATGGAACATGACAGTTAT 700
 Db 181 CTCCACAGTTTGTATGCTGTCACAAAGCAGAGTGTTATCAGCTCATGGAACACGACGTAT 240

RESULT 11
 ADD34052
 ID ADD34052 standard; DNA; 681 BP.
 XX
 AC ADD34052;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX Mouse mitochondrial DNA sequence SEQ ID NO:1828.
 DE
 DE 1..240
 XX
 KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
 KW mitochondrial disease; oxidative phosphorylation dysfunction;
 KW oxidative stress; apoptosis; aging.
 XX
 OS Mus musculus.
 XX
 XX WO2003020220-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 30-AUG-2002; 2002WO-US027886.
 XX
 PR 30-AUG-2001; 2001US-0316323P.
 PR 31-AUG-2001; 2001CA-02356540.
 XX
 XX (UYEM-) UNIV EMORY.
 XX
 XX Wallace DC, Levy S, Kerstann K, Procaccio V;
 PI WPI; 2003-300821/29.
 DR
 DR
 XX
 XX Array containing probes for genes involved in mitochondrial biology,
 PT useful for determining mitochondrial biology gene expression profiles for
 PT use in diagnosing pathologies and identifying biochemical pathways.
 XX
 PS Claim 2; SEQ ID NO 1828; 201pp; English.
 XX
 XX The invention relates to a novel array comprising at least two isolated
 CC nucleotide molecules, each molecule having a sequence capable of uniquely
 CC hybridising to a nucleic acid molecule which is an expression product of
 CC a gene involved in mitochondrial biology. The array comprises two or more
 CC isolated nucleic acid molecules or spots, each molecule having a sequence
 CC chosen from sequence of 994 human probes and 2046 mouse probes. An array
 CC of the invention is useful for determining an expression profile of a
 CC mouse or human sample containing nucleic acid, by contacting the array
 CC with the sample under conditions allowing selective hybridisation, and
 CC measuring hybridisation of nucleic acid in the sample to the array to
 CC produce an expression profile. The array is also useful for determining
 CC an expression profile of a first labelled sample containing nucleic acid
 CC relative to a second, differently labelled sample containing nucleic
 CC acid. The second sample is a reference or a standard. An array is useful
 CC for determining an expression profile diagnostic of an energy-metabolism-
 CC related physiological condition. An array of the invention is useful for
 CC determining mitochondrial biology gene expression profiles of organisms,
 CC such as human, mice and closely related species, tissue and organs of

CC such organisms, which are useful for determining expression profiles
CC diagnostic of energy metabolism-related physiological conditions,
CC diagnosing such physiological conditions, identifying biochemical
CC pathways, genes, and mutations involved in such physiological conditions,
CC identifying therapeutic agents useful for preventing and/or treating such
CC physiological conditions, evaluating and/or monitoring the efficacy of
CC such therapies, and creating and identifying animal models of human
CC energy metabolism-related physiological conditions. An array is also
CC useful for defining expression signatures or profiles for mitochondrial
CC diseases, as well as distinguishing clinical disorders that result from
CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
CC apoptosis and aging. An array of the invention contains probes of genes
CC not previously recognised to participate in mitochondrial biology. The
CC sequences shown in ADD3224-ADD3260 represent murine mitochondrial DNA
CC clones used to make the probes of the invention. Some sequences are not
CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
CC 1906, 2408 and 2643.

XX SQ Sequence 681 BP; 217 A; 164 C; 157 G; 143 T; 0 U; 0 Other;
Query Match 13.4%; Score 156.2; DB 9; Length 681;
Best Local Similarity 64.0%; Pred. No. 1.1e-24;
Matches 236; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 359 TCTCTGAGAGCAGTGAATGGGCTGAATCATTTGACAAATGCTCTCATAGAGAT 418
DB 220 TCTCTGAGAGCAGTGAATGGGCTGAATCATTTGACAAATGCTCTCATAGAT 418
QY 419 GGAGTGGATGTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAGCAATTTGAAATTT 478
DB 280 GGGCTGGCTGATTCAGCGGGCTTTTAAAGTCCAGTTCTGTGAAGAAACATTTGAAATTC 339
QY 479 TGGTTCGCTGTGAAGACTTCAAGAAATGCAAGAACTCAACAAATCATCTTAAAGCA 538
DB 340 TGGTTCGCTGTGAAGACTTCAAGAAATGCAAGAACTCAACAAATCATCTTAAAGCA 538
QY 539 AAGCGAATCTATGAGAAATTCATTCAGATCATGCCCAAGAGGTTTAAATGATTTT 598
DB 400 AGGAATATCTATACCGATTCATGAGAGAGAGCTCCCAAGAGATATACATAGACTTC 459
QY 599 CATACTAAGAGAGTAAATGCTAAGAGCATGCCCGCCCACTCTCCACAGTTTGTATCG 658
DB 460 CAACGAAATCTCTGATTTGCCCAAAATATCCAGAGGCTACAGTGGCTGTTCCACACA 519
QY 659 GCACAAAGCAGGTGTACAGCTCATGCAACATGACAGTTTAAACGCTTTTGAATCT 718
DB 520 GCTCAGAGAGGGTGTACAGTTGATGAGAAACAATTCCTATCTCTGCTTCTTGAGTCC 579
QY 719 GAGACCTTAC 727
DB 580 GAATTCATAC 588

RESULT 12
ABT10881
ID ABT10881 standard; cDNA; 1345 BP.
XX ABT10881;
AC ABT10881;

XX 04-DEC-2002 (first entry)
DT Human breast cancer associated coding sequence SEQ ID NO: 1015.
DE Human breast cancer associated coding sequence SEQ ID NO: 1015.
XX Human; breast specific gene; breast cancer; differential expression;
KW cytostatic; gene therapy; gene; ss.
XX Homo sapiens.
XX WO200259271-A2.
XX 01-AUG-2002.
XX 25-JAN-2002; 2002WO-US002176.

XX 25-JAN-2001; 2001US-0263757P.
PR 23-APR-2001; 2001US-0286909P.
PR 23-MAY-2001; 2001US-0292517P.
XX (GENE-) GENE LOGIC INC.
XX Orr MS, Nation M, Diggins JC, Zeng W;
XX WPI; 2002-674803/72.
XX Diagnosing breast cancer in a patient comprises detecting the level of
PT gene expression in cell or tissue samples, where a differential gene
PT expression is indicative of breast cancer.

XX Claim 1; SEQ ID NO 1015; 260pp + Sequence Listing; English.

XX The present invention relates to methods of diagnosing breast cancer in a
CC patient, which comprise detecting the level of expression in a tissue
CC sample of two or more genes selected from those shown in ABT09867-
CC ABT1112, where a differential expression of the genes indicates breast
CC cancer. The methods are useful in diagnosing, treating, detecting the
CC progression, and in monitoring treatment of breast cancer in patients.
CC The methods are also useful as a screening tool for agents that modulate
CC the onset or progression of breast cancer. The breast cancer genes may be
CC used as diagnostic markers for the prediction or identification of the
CC malignant state of breast tissue, for confirming the type and progression
CC of cancer, and for drug screening and assays. The present sequence is a
CC coding sequence of the invention. Note: the sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub.published_pct_sequences

XX SQ Sequence 1345 BP; 443 A; 254 C; 304 G; 344 T; 0 U; 0 Other;
Query Match 13.1%; Score 152.4; DB 6; Length 1345;
Best Local Similarity 62.7%; Pred. No. 8.7e-24;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 359 TCTCTGAGAGCAGTGAATGGGCTGAATCATTTGACAAATGCTCTCATAGAGAT 418
DB 249 TCTCTGAGAGCAGCTGTGGTCAGAGCATTTCAGAGCTGCTAGCCAGCAATAT 308
QY 419 GGAGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAGCAATTTGAAATTT 478
DB 309 GGTCTTGTGCTATTCAGGGCTTTTAAAGTCCGAAATCTGTGAAGAAATATTTGAATTC 368
QY 479 TGGTTCGCTGTGAAGACTTCAAGAAATGCAAGGACCTCAACAAATCATCTTAAAGCA 538
DB 369 TGGTTCGCTGTGAAGACTTCAAGAAATGCAAGGACCTCAACAAATCATCTTAAAGCA 428
QY 539 AAGCGAATCTATGAGAAATTCATTCAGATCATGCCCGCCCAAGAGGTTTAAATGATTTT 598
DB 429 AGGAATATCTATACCGATTCATGAGAGAGAGCTCCCAAGAGATATACATAGATTTT 488
QY 599 CATACTAAGAGAGTAAATGCTAAGAGCATGCCCGCCCACTCTCCACAGTTTGTATCG 658
DB 489 CAAACCAAACTCTGATTTGCCAGAAATATACAAAGAGCTACAGTGGCTGCTTACAACT 548
QY 659 GCACAAAGCAGGTGTACAGCTCATGGAACATGACAGTTTAAACGCTTTTGAATCT 718
DB 549 GCCGAGAAAGGGTATACAGCTTGAAGAGAAACAATCTATCTCTGTTCTTGGAGTCA 608
QY 719 GAGACCTTACTTACATTTG 736
DB 609 GAATTCATACAGGACTTG 626

RESULT 13
ABK83834
ID ABK83834 standard; cDNA; 1345 BP.
XX ABK83834;
AC ABK83834;

XX DT 14-AUG-2002 (first entry)

XX DE Human cDNA differentially expressed in granulocytic cells #405.

XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;

XX KW viral infection; parasitic infection; protozoal infection;

XX KW fungal infection; sterile inflammatory disease; psoriasis;

XX KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

XX KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

XX KW adult respiratory distress syndrome; inflammatory bowel disease;

XX KW Crohn's disease; ulcerative colitis; periodontal disease;

XX KW granulocyte activation; chronic inflammation; allergy.

XX OS Homo sapiens.

XX PN WO200228999-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX DR WPI; 2002-435328/46.

XX PT Detecting granulocyte activation by detecting differential expression of

XX PT genes associated with granulocyte activation, which serves as diagnostic

XX PT markers that is useful for monitoring disease states and drug toxicity.

XX PS Claim 1; SEQ ID NO 405; 114pp; English.

XX CC The invention relates to detecting (M1) granulocyte (GC) activation

XX CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

XX CC DNA chip analysis as given in the specification, and comparing the

XX CC expression level to an expression level in an unactivated GC, where

XX CC differential expression of Gs is indicative of GCA. Also included are

XX CC modulating (M2) GAs by contacting GC with an agent that alters the

XX CC expression of at least one gene in Gs; (2) screening (M3) for an agent

XX CC capable of modulating GCA or an inflammation (especially chronic) in a

XX CC tissue, an allergic response in a subject, exposure of a subject to a

XX CC pathogen or sterile inflammatory disease using the gene expression

XX CC profile; (3) detecting (M4) an inflammation (especially chronic) in a

XX CC tissue, an allergic response in a subject, exposure of a subject to a

XX CC pathogen or sterile inflammatory disease, by detecting the level of

XX CC expression in a sample of the tissue of gene(s) from Gs, where the level

XX CC of expression of the gene is indicative of inflammation; (4) treating

XX CC (M5) an inflammation (especially chronic) or in a tissue, an allergic

XX CC response in a subject, exposure of a subject to a pathogen or sterile

XX CC inflammatory disease, by contacting a tissue having inflammation with an

XX CC agent that modulates the expression of gene(s) from Gs in the tissue. M1

XX CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful

XX CC for screening an agent capable of modulating GCA preferably in an

XX CC inflammation in a tissue; M4 is useful for detecting an inflammation

XX CC (especially chronic) in a tissue, an allergic response in a subject,

XX CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.

XX CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,

XX CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult

XX CC respiratory distress syndrome, inflammatory bowel disease, Crohn's

XX CC disease, ulcerative colitis, periodontal disease; also bacterial

XX CC infection, viral infection, parasitic infection, protozoal infection,

XX CC fungal infection and M5 is useful for treating one of the above

XX CC conditions. The present sequence represents a gene differentially

XX CC expressed in granulocytes. Note: The sequence data for this patent did

XX CC not form part of the printed specification, but was obtained in

XX CC electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published_pat_sequences

XX CC Sequence 1345 BP; 443 A; 254 C; 304 G; 344 T; 0 U; 0 Other;

Query Match 13.1%; Score 152.4; DB 6; Length 1345;
Best Local Similarity 62.7%; Pred. No. 8.7e-24;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 359 TCTCTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCATAGAGAT 418
DB TCTCTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCATAGAGAT 418
QY 249 TCTCTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCATAGAGAT 308
DB TCTCTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCATAGAGAT 308
QY 419 GGAGTGGATGCTTTTACCAAGATTTCTTAAAGTGAATTCAGTGAGGAGAACATTTGAATTT 478
DB GGATTTGCTGCATTCAGGCTTTTAAAGTGGAAATTCGTGAAGAAAATATTGAATTC 368
QY 479 TGGTGGCTGTGAAGACTTCAAGAAATGCAAGAGACCTCAACAATCATCTCTAAAGCA 538
DB TGGTGGCTGTGAAGACTTCAAGAAATGCAAGAGACCTCAACAATCATCTCTAAAGCA 428
QY 539 AAGGCAATCTATGAGAAATTCATTGAGATGATGCCCCCAAGAGGTTAAACATTTGATTT 598
DB AAGGCAATCTATGAGAAATTCATTGAGATGATGCCCCCAAGAGGTTAAACATTTGATTT 598
QY 429 AGGAAATATATCTACTGACTTCATAGAAAGAGAGCTCCAAAGAGATAAACATAGATTT 488
DB AGGAAATATATCTACTGACTTCATAGAAAGAGAGCTCCAAAGAGATAAACATAGATTT 488
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DB CAATCCAAAGTCTGATTTGCCAGAAATATACAAGAGGCTACAAAGTGGCTTTTACAAT 548
QY 659 GCACAAAGCAGAGTGTACCAGCTCATGGAACATGACAGTTATATAACGCTTTTGAATCT 718
DB GCCCAGAAAGGATATACAGTTGATGAGAACAACTCTTATCTCTGTTTCTGGAGTCA 608
QY 719 GAGACTACTTACATTTG 736
DB GAATTTCTACAGGACTTG 626

RESULT 14
ACC46750
ID ACC46750 standard; cDNA; 1345 BP.
XX ACC46750;
XX AC
XX DT 05-JUN-2003 (first entry)
XX DE Human COPD related protein encoding cDNA SEQ ID NO:1.
XX KW Human; chronic obstructive pulmonary disease; COPD; chronic lung disease;
XX KW gene; ss.
XX OS Homo sapiens.
XX PN WO200297127-A2.
XX PD 05-DEC-2002.
XX PF 28-MAY-2002; 2002WO-EP005835.
XX PR 31-MAY-2001; 2001GB-00013266.
XX PA (FARB) BAYER AG.
XX PI Oellers N, Gehrman M, Kallabis H, Hall R, Schulze T, Kroegel C;
XX WPI; 2003-140492/13.
XX P-PSDB; ABP96779.
XX PT Predicting, diagnosing or prognosing chronic lung disease, by detecting a
XX PT chronic obstructive pulmonary disease (COPD) gene in a biological sample.
XX PS Claim 8; Page 73-74; 214pp; English.
XX CC The present invention describes a method for predicting, diagnosing or
XX CC prognosing chronic lung disease by detecting a chronic obstructive
XX CC pulmonary disease (COPD) gene related polynucleotide (see ACC46750 to
XX CC ACC46777, which encode the COPD related proteins in ABP96779 to

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2004, 05:14:44 ; Search time 92.2662 Seconds
(without alignments)
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Title: US-09-894-749-3

Perfect score: 1164

Sequence: 1 tttttgaagaaaaatctga.....gtactagtgcgcgagctc 1164

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1164	100.0	1164	4	US-09-498-959-3
3	596	51.2	2217	3	US-09-244-314-1
4	596	51.2	2217	4	US-09-498-959-1
5	305.4	26.2	736	4	US-09-833-381-1010
6	152.4	13.1	1345	4	US-09-016-434-1278
7	152.4	13.1	1345	4	US-09-023-655-1243
8	142	12.2	744	2	US-08-748-483-2
9	142	12.2	2190	4	US-09-023-655-795
10	139	11.9	800	4	US-09-016-434-1091
11	136	11.7	3208	4	US-09-568-921-111
12	132.6	11.4	2638	4	US-09-016-434-1090
13	129.8	11.2	1398	4	US-09-016-434-1290
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20	122.6	10.5	606	2	US-08-461-379A-27
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25	122.6	10.5	746	3	US-08-870-815-3
26	122.6	10.5	746	3	US-08-949-004-3
27	122.6	10.5	2383	1	US-08-274-318-1

RESULT 1
US-09-244-314-3
; Sequence 3, Application US/09244314
; Patent No. 6274362
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174690
; CURRENT APPLICATION NUMBER: US/09/244,314
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)..(841)
; US-09-244-314-3

Query Match 100.0%; Score 1164; DB 3; Length 1164;
Best Local Similarity 100.0%; Pred. No. 2.7e-285;
Matches 1164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTTTTGTAGAAAAATCTGAGGAAGATTGGGATAGCGCTTTATTTCAGGATGTTTTCT	60	Sequence 1, Appli
Db	1	TTTTTGTAGAAAAATCTGAGGAAGATTGGGATAGCGCTTTATTTCAGGATGTTTTCT	60	Sequence 1, Appli
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Qy	121	ACTGGACAGAAATATGATATGATCTGCTTCTCTCAATTAATATGTTGAATC	180	Sequence 4, Appli
Db	121	ACTGGACAGAAATATGATATGATCTGCTTCTCTCAATTAATATGTTGAATC	180	Sequence 4, Appli
Qy	181	AAAAGAGAAAACTTTTTCAACTAATGATGGGTGAGGAAAGAAAGAAACAGCATCGA	240	Sequence 240, Appli
Db	181	AAAAGAGAAAACTTTTTCAACTAATGATGGGTGAGGAAAGAAAGAAACAGCATCGA	240	Sequence 240, Appli
Qy	241	GGCCAAATCAGAGCGAAAGAAAAGAAATAGACTTAAGTCTTCTCTCAGAGGCTGA	300	Sequence 42, Appli
Db	241	GGCCAAATCAGAGCGAAAGAAAAGAAATAGACTTAAGTCTTCTCTCAGAGGCTGA	300	Sequence 42, Appli
Qy	301	CTTCCATGGAGAGACTCAAGCCAGTAGACTCGCCCTCTTGGCCAAAGAAACAGAGTCTC	360	Sequence 42, Appli
Db	301	CTTCCATGGAGAGACTCAAGCCAGTAGACTCGCCCTCTTGGCCAAAGAAACAGAGTCTC	360	Sequence 42, Appli

ALIGNMENTS

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361 TCCTGAAGACAGTGAATGGCTGAATCATTTGACAAATTTGCTCTCTCATAGAGTGG 420
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Mus sp.
421 AGTGATGCTTTTACAGATTTCTTAAACAGTAACTAGTGAAGAGAACATTTGAATTTTG 480
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)...(841)
421 AGTGATGCTTTTACAGATTTCTTAAACAGTAACTAGTGAAGAGAACATTTGAATTTTG 480
US-09-498-959-3
481 GGTGCGCTGTGAAGACTTCAAGAAATGCAAGAACTCAACAAATCATCTCTTAAAGCAAA 540
Query Match 100.0%; Score 1164; DB 4; Length 1164;
Best Local Similarity 100.0%; Pred. No. 2.7e-285; Indels 0; Gaps 0;
Matches 1164; Conservative 0; Mismatches 0;
481 GGTGCGCTGTGAAGACTTCAAGAAATGCAAGAACTCAACAAATCATCTCTTAAAGCAAA 540
541 GGCATCTATGAGAAATTCATTCAGAAATGATGCCGCCCAAGAGGTTAACATTTGCTCA 600
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RESULT 2

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US-09-498-959-3
; Sequence 3, Application US/09498959
; Patent No. 6410240
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5800-19A
; CURRENT APPLICATION NUMBER: US/09/498,959
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: 09/244,314
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 3
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)...(841)
US-09-498-959-3
Query Match 100.0%; Score 1164; DB 4; Length 1164;
Best Local Similarity 100.0%; Pred. No. 2.7e-285; Indels 0; Gaps 0;
Matches 1164; Conservative 0; Mismatches 0;
QY 1 TTTTGTAAAGAAATCTCGAGAAAGATTCGGGATAGCGCTTTATTCAGGATGTTTCT 60
DB 1 TTTTGTAAAGAAATCTCGAGAAAGATTCGGGATAGCGCTTTATTCAGGATGTTTCT 60
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301 CTTCCATGGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAAGAAAGAGT 360
361 TCTGTGAAGAGCAGTGAATGGCTGAAATCTTCAAGAAATGCTCTCTCATAGAGTGG 420
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421 AGTGGATGCTTTTACAGATTTCTTAAACAGTAACTCAAGTGAAGTGAAGTGAAGTGA 480
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541 GGCATCTATGAGAAATTCATTCAGAAATGATGCCGCCCAAGAGGTTAACATTTGCTCA 600
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Db	961	ACACCATGCAAAATACATATTAAATGTTAAGAACTTTTATATTATCTAATAAATAATTCTATC	1020
Qy	1021	ATCTATCTTCCGAAATATTTTATGAAAAATCTATCTGATATTCTATTCTTAATAAAATCTTT	1080
Db	1021	ATCTATCTTCCGAAATATTTTATGAAAAATCTATCTGATATTCTATTCTTAATAAAATCTTT	1080
Qy	1081	TATTTCTACAAATACAGTTCAGTAGAAGAAGCTTTTGAAGCCGAATTCAGCACACTGGCG	1140
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Qy	1141	GC CGGTACTAGTGGATCCGAGCTC	1164
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RESULT 3
 US-09-244-314-1
 ; Sequence 1, Application US/09244314
 ; Patent No. 6274362
 ; GENERAL INFORMATION:
 ; APPLICANT: Hodge, Martin R.
 ; APPLICANT: Yonge, David
 ; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
 ; FILE REFERENCE: 5800-19, 035800/174680
 ; CURRENT APPLICATION NUMBER: US/09/244,314
 ; CURRENT FILING DATE: 1999-02-04
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 2217
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (160)..(867)
 ; US-09-244-314-1

Query Match	51.2%;	Score 596;	DB 3;	Length 2217;
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Qy	281	CTTCTCTCTACAGAGCCCTGACCTTCATGGAGAGACTCAAGCCAGTAGACTCGCCCTCTTG	340	
Db	307	CTTCTTGTGCGAAACCTGAGTTTCATGAAGCACCCGCTCCAGTAGACTCTGGGCACATG	366	
Qy	341	GCCAAAGAAACAAGAGTCTCTCCTCAAGAACAGTGAATGGGCTGAATCATTTGACAAA	400	
Db	367	GCCAAAGAAACAAGAGTCTCTCCCTGAAGAGGAGTGAATGGGCTGAATCATTTGACAAA	426	
Qy	401	TTGCTCTCTCTACAGATGGAGTGGATGCTTTTACCAGATTCTTTAAAACTGAATTCAGT	460	

Db	427	CTGCTTTCCCATAGAGATGGACTAGAGGCTTTTACAGATTTTCTTAAACTGAATTCAGT	486
Qy	461	GAGGAGAAACATTGAAATTTTGGGTGGCTGTGAAGACTTCAAGAAATGCANGAGAACTCAA	520
Db	487	GAAAGAAAATATTGAAATTTTGGATAGGCTGTGAAGATTTCAAGAAAAACAAGGACCTCAA	546
Qy	521	CAAAATCATCTTAAAGCAAAAGCAATCTATGAGAAATTCATTCCAGAAATGATGCCCCAAA	580
Db	547	CAAAATTCACCTTAAAGCAAAAAGCAATATATGAGAAATTTATACAGAGTGAATGCCCAAAA	606
Qy	581	GAGGTTAAACATTCGATTTTTCATCTAAAGAGTAAATTCGTTAAGAGACATCGCCAGCCCACT	640
Db	607	GAGGTTAAACCTTGATTTTTCACAAAAGAAGTCAATTACAAAAGCATCACTCAACCTACC	666
Qy	641	CTCCACAGTTTTGATACGGCACAAAGCAGAGTGTACAGCTCATGGAACATGACAGTTAT	700
Db	667	CTCCACAGATTTTCATGCTGCACAAAGCAGAGTGTATCAGCTCATGGAACCAAGACAGTTAT	726
Qy	701	AAAGCTTTTTTGAAATCTGAGACCTACTTACATTTGATAGAAAGGAACCTCAGAGACCA	760
Db	727	ACAGTTTTCTGAAATCTGACATCTATTAGACTTGTGATGGAAGAGACCTCAGAGACCA	786
Qy	761	ACAAACCTTAGGAGACGATCAGCATCAATTTACTTTTCAATGATTTCCNAGATGTAAAGTCA	820
Db	787	ACAAATCTTAGGAGACGATCACGCTCATTTTACCTGCAATGAATCCAAAGATGTACAATCA	846
Qy	821	GATGTTGCCATTTGGTTATCAGTAAAGAGTCATTTGTCTCTTTTGTAGTGTATGTGTAT	880
Db	847	GATGTTGCCATTTGGTTATTAAGAAAATTCATTTTGTCTCATTTTATGACAAAACCTTATAC	906
Qy	881	ATCTAAATAATATACATAACTAATGTGTACTTCTTAAATAATAGCTTGTGTATAAGAGA	940
Db	907	ATC-----TGCTTCTAACATATCGATTCGATTTTATGCTTTAAGA	941
Qy	941	GATGATTTTCATTTT-----TAAATAACCATGCAAAATACATATTAATGTATAAGAACTT	994
Db	942	TTTGGTCCCATCTTTTAAACTGAAATATGTCAATGAAATATTTTAAAAATGTAAAAAC	1001
Qy	995	TTTATATATACATAAATAATTCATCATCTATCTTCGAAATAATTTTATGAAATCTATC	1054
Db	1002	AAAACCTTCTGCTACAAAATACATACAGTATCTGCCAGTATATCTCTGTAAACCTTCTA	1061
Qy	1055	TGATATCTTATCTPAATAAAATTC	1078
Db	1062	TTTGAATGCTCATTTCAATTTATAATC	1085

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RESULT 4
US-09-498-959-1
; Sequence 1, Application US/09498959
; Patent No. 6410240
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5800-19A
; CURRENT APPLICATION NUMBER: US/09/498,959
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: 09/244,314
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2217
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)... (857)
US-09-498-959-1

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Query Match

Best Local Similarity 75.8%; Pred. No. 1.9e-141;
Matches 791; Conservative 0; Mismatches 220; Indels 33; Gaps 3;

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QY 41 TTATTCAGGATGTTTCTCTATGAATAGCATTCATCTGTGGGAGAGAGAGGACTAAGG 100
Db 69 TTATTCAGGATGTTTCTCTATGAATAGCATTCATCTGTGGGAGAGAGAGGACTAAGG 128
QY 101 AAATCTGACATCTGTTGGTCACTCGGACAGATATGGATATGTCACCTGGTTTCTTCTCT 160
Db 129 AAATAGACATCTTTCAT--TTTAGAGAGAGATGGAAACACATGCTTTTCTTCTCT 186
QY 161 CAATTAATATGTTGAATCAAAAGAGAAACTTTTTTCAAACTAATGTCATGGTTCAGGG 220
Db 187 CAATTAATATGTTGAATCAAAAGAGAAACTTTTTTCAAACTAATGTCATGGTTCAGGA 246
QY 221 AAAGAAGAAACAGCATCGAGCCCAAAATCGAGCGGAAGAAAGAAAGAAATAGACTAAGT 280
Db 247 AAAGAAGAAACAGCAAGAACCAAAATCGAGCTAAGGAAGAAAGAAATAGACTAAGT 306
QY 281 CTTCTCTACAGAGCCCTGACTTCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTG 340
Db 307 CTTCTCTACAGAGCCCTGACTTCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTG 366
QY 341 GCCAAGAAACAGAGTCTCTCTGAAGACAGTGAATGGCTGAATCATTTGACAAA 400
Db 367 GCCAAGAAACAGAGTCTCTCTGAAGACAGTGAATGGCTGAATCATTTGACAAA 426
QY 401 TTGCTCTCTACAGAGTGGAGTGGATGCTTTTACCAGATTTCTTAAACTGAAATTCAGT 460
Db 427 CTGCTTTCCCATAGAGTGGAGTGGATGCTTTTACCAGATTTCTTAAACTGAAATTCAGT 486
QY 461 GAGGAGACATGAAATTTTGGTTCGCTGTGAAGACTTCAAGAAATGCAAGAACCTCAA 520
Db 487 GAAGAAATATGAAATTTTGGTTCGCTGTGAAGACTTCAAGAAATGCAAGAACCTCAA 546
QY 521 CAATTCATCTTAAAGCAAGCAATCTATGAGAAATTCATTGAGATGATGCCCCAAA 580
Db 547 CAATTCATCTTAAAGCAAGCAATCTATGAGAAATTCATTGAGATGATGCCCCAAA 606
QY 581 GAGGTAACATGATTTTCACTAAGAAAGTAATGCTAAGAGCATGCGCCAGCCCACT 640
Db 607 GAGGTAACATGATTTTCACTAAGAAAGTAATGCTAAGAGCATGCGCCAGCCCACT 666
QY 641 CTCACAGTTTGTATCGGCAAGAGAGTGTACAGCTCATGGAACATGACAGTTAT 700
Db 667 CTCACAGTTTGTATCGGCAAGAGAGTGTATCAGCTCATGGAACATGACAGTTAT 726
QY 701 AAACGCTTTTGAATCTGAGACCTACTTACATTTGATAGAAGAGACCTCAGAGACCA 760
Db 727 ACACGTTTCTGAAATCTGACATCTATTTAGACTTGTATGGAAGAGACCTCAGAGACCA 786
QY 761 ACNACCTTAGAGAGATCAGATCATTTTACTTACATGATTTTCCAGATGTAAGTCA 820
Db 787 ACNACCTTAGAGAGATCAGATCATTTTACTTACATGATTTTCCAGATGTAAGTCA 846
QY 821 GATGTTGCCATTTGTTATGAGTAAAGTCAATTTGCTCTTTTGTAGTGTATGCTAT 880
Db 847 GATGTTGCCATTTGTTATGAGTAAAGTCAATTTGCTCTTTTGTAGTGTATGCTAT 906
QY 881 ATCTAAATATATACATACTAATGTTGACTTCTTAAATATAGCTTGTGTATAGAGA 940
Db 907 ATC-----TGCTTCTAATATGCTGTTTATGTTTAAAG 941
QY 941 GATGATTTCAITTTT-----TAAATACACCATCAATATATATTAATGTAAGACTT 994
Db 942 TTTGTTCCATCTTAACTGAATATGCTGATGAAATTTTAAATGTAAGACTT 1001
QY 995 TTTATATATATAAAATATATATATATATATATATATATATATATATATATATATAT 1054
Db 1002 AAAAATTTCTGTAACAAATATATATATATATATATATATATATATATATATATAT 1061
QY 1055 TGATATTTCTATTTAATAAATTC 1078
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Db 1062 TTTGATGTCATTCATTCATTTATAATC 1085

RESULT 5

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US-09-833-381-1010
; Sequence 1010, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1010
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(736)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1010
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Query Match 26.2%; Score 305.4; DB 4; Length 736;
Best Local Similarity 86.8%; Pred. No. 4.5e-68;
Matches 336; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 455 TTCAGTGAGAGAGCAATTTGTTGGTGGCTGTGAGAGCTTCAAGAAATGCAAGGAA 514
Db 4 TTCAGTGAGAGAGCAATTTGTTGGTGGCTGTGAGAGCTTCAAGAAATGCAAGGAA 63
QY 515 CCTCAACAAATCATCTTAAAGCAAGGCAATCTATGAGAAATTCATTGAGATGATGCC 574
Db 64 CCTCAACAAATTCACCTTAAAGCAAGCAATATATGAGAAATTTATACAGCTGATGCC 123
QY 575 CCAAGAGAGGTTAAAGTTTCACTACTAAAGAAATTTGCTTAAAGAGATGCCCGAG 634
Db 124 CCAAGAGAGGTTAAAGTTTCACTACTAAAGAAATTTGCTTAAAGAGATGCCCGAG 183
QY 635 CCACCTCTCCAGTTTGTATGACGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 694
Db 184 CCACCTCTCCAGTTTGTATGACGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 243
QY 695 AGTTATAAAGCGCTTTTGAATCTGAGACCTACTTACATTTGATAGAAGAGAGAGAG 754
Db 244 AGTTATAAAGCGCTTTTGAATCTGAGACCTACTTACATTTGATAGAAGAGAGAGAG 303
QY 755 AGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
Db 304 AGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
QY 815 AAGTCAGAGAGTTGCCATTTGGTTATCA 841
Db 364 CAATCAGAGTTGCCATTTGGTTATCA 390
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RESULT 6

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US-09-016-434-1278
; Sequence 1278, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
```

CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1278:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G292054
US-09-016-434-1278

Query Match 13.1%; Score 152.4; DB 4; Length 1345;
Best Local Similarity 62.7%; Pred. No. 3e-29;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

Qy	359	TCTCTGAGAGCAGTGAATGGCTGAATTCATTTGACAAATTCCTCTCATAGAGAT	418
Db	249	TCTCTGAGAGCAGCAGCTGTGTCAGAACATTTGACGAGCTGCTAGCCAGCAATAT	308
Qy	419	GGAGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGGAGCAATTTGAATTT	478
Db	309	GGTCTGCTGCATTCAGGGCTTTTAAAGTCGGAATTCCTGAAGAAATATTGAATTC	368
Qy	479	TGGTGGCTGTGAAGACTTCAAGAAATGCAAGAACCTCAACAAATCATCTTAAAGCA	538
Db	369	TGGTGGCTGTGAAGACTTCAAAAAACCAATCACCCCAAAAGCTGTCTCAAAAGCA	428
Qy	539	AAGCAATCTATGAGAAATTCATTGAGATGATGCCCCCAAGAGGTTAACTTTGAATTT	598
Db	429	AGGAATATATATCTGACTTCATAGAAAGGAGCTCCAAAGAGATATAACATAGATTT	488
Qy	599	CATACCTAAAGAGTAATTTGCTAAGACATGCCCCAGCCACTCTCCACAGTTTGTACG	658
Db	489	CAAAACCAAACTCTGATTCGCCAGAAATATACAAGAGCTACAAGTGGCTGTCTTACAACT	548
Qy	659	GCACAAAGCAGTGTACAGCTCATGGAATGAGATGAGCTTATAACGCTTTTGAATCT	718
Db	549	CCCCAGAAAGGGTATACAGCTTGATGAGAACAACTCTTATCTCTCTTCTTGAGTCA	608
Qy	719	GAGACCTACTTACATTTG 736	
Db	609	GAATTCACAGGACTTG 626	

RESULT 7
US-09-023-655-1243
Sequence 1243, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1243:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G292054
US-09-023-655-1243

Query Match 13.1%; Score 152.4; DB 4; Length 1345;
Best Local Similarity 62.7%; Pred. No. 3e-29;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

Qy	359	TCTCTGAGAGCAGTGAATGGCTGAATTCATTTGACAAATTCCTCTCATAGAGAT	418
Db	249	TCTCTGAGAGCAGCAGCTGTGTCAGAACATTTGACGAGCTGCTAGCCAGCAATAT	308
Qy	419	GGAGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGGAGCAATTTGAATTT	478
Db	309	GGTCTGCTGCATTCAGGGCTTTTAAAGTCGGAATTCCTGAAGAAATATTGAATTC	368
Qy	479	TGGTGGCTGTGAAGACTTCAAGAAATGCAAGAACCTCAACAAATCATCTTAAAGCA	538
Db	369	TGGTGGCTGTGAAGACTTCAAAAAACCAATCACCCCAAAAGCTGTCTCAAAAGCA	428
Qy	539	AAGCAATCTATGAGAAATTCATTGAGATGATGCCCCCAAGAGGTTAACTTTGAATTT	598
Db	429	AGGAATATATATCTGACTTCATAGAAAGGAGCTCCAAAGAGATATAACATAGATTT	488
Qy	599	CATACCTAAAGAGTAATTTGCTAAGACATGCCCCAGCCACTCTCCACAGTTTGTACG	658
Db	489	CAAAACCAAACTCTGATTCGCCAGAAATATACAAGAGCTACAAGTGGCTGTCTTACAACT	548
Qy	659	GCACAAAGCAGTGTACAGCTCATGGAATGAGATGAGCTTATAACGCTTTTGAATCT	718
Db	549	CCCCAGAAAGGGTATACAGCTTGATGAGAACAACTCTTATCTCTCTTCTTGAGTCA	608
Qy	719	GAGACCTACTTACATTTG 736	

Db 609 GAATTCACAGGACTTG 626
|| |||||
RESULT 8
US-08-748-483-2
; Sequence 2, Application US/08748483
; Patent No. 595314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J. 36,749
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0157 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 57362
; US-08-748-483-2
Query Match 12.2%; Score 142; DB 2; Length 744;
Best Local Similarity 59.8%; Pred. No. 1e-26;
Matches 238; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 341 GCCAAGAAACAAGAGTCTCTCCTGAGAACAGTGAATGGGCTGAATCAATTGACAAA 400
|||
Db 210 GCCAAGACCCAGAAAACCTCGTGACGAGGCCCTGCGAGTGGCGTGATTCCTCGACAAA 269
|||
QY 401 TTGCTCTCTCAGAGATGGAGTGGATGCTTTTACCAGATTCTTAAACTGAATTCAGT 460
|||
Db 270 CTCCTGCGAGAACACTATGAGCTTCCGAGTTTCAAAAGTTTCTTGAAGTGAATTCAGT 329
|||
QY 461 GAGGAGAACATGTAATTTTGGTGGCTCGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAA 520
|||
Db 330 GAGGAAAACCTTGAATTTGCTGAGTTCCTGTGAGGATTACAAGAGATCAAGTCCCTGCC 389
|||
QY 521 CAATCATCTTAAAGCAAGCAATCTATCAGAAATTCATTCAGATGATGCCCCAAA 580
|||
Db 390 AAGATGCGTGAGAGGCAAGCAAAATTTATGAAGATTCATTCAACGAGGCTCTTAAA 449
|||
QY 581 GAGGTTAAACATTTTTCATCTACTAAAGAGTAATTTGCTAAGAGCATCGCCCGAGCCCACT 640
|||

Db 450 GAGTGGAATATTGACCACTTCACTAAGGACATCAATGAAGAACTGGTGGAACTTCC 509
QY 641 CTCACAGTTTTGATACGGCACAAGCAGAGTGTACCACTCATGGAACATGACAGTTAT 700
|||
Db 510 CTGAGCAGCTTTGACATGCCCCAGAAAAGATCCATGCCCTCATGGAAGGATTTCTG 569
|||
QY 701 AAAGCTTTTGAATCTCGAGACCTACTTACATTTGAT 738
|||
Db 570 CCTCGCTTTGCGCTCTGAGTTTATATCAGGAGTTAAT 607
|||

RESULT 9
US-09-023-655-795
; Sequence 795, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 795:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2190 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAT03
; CLONE: 696878
; US-09-023-655-795
Query Match 12.2%; Score 142; DB 4; Length 2190;
Best Local Similarity 59.8%; Pred. No. 1.5e-26;
Matches 238; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 341 GCCAAGAAACAAGAGTCTCTCCTGAGAACAGTGAATGGGCTGAATCAATTGACAAA 400
|||
Db 210 GCCAAGACCCAGAAAACCTCGTGACGAGGCCCTGCGAGTGGCGTGATTCCTCGACAAA 269
|||
QY 401 TTGCTCTCTCAGAGATGGAGTGGATGCTTTTACCAGATTCTTAAACTGAATTCAGT 460
|||
Db 270 CTCCTGCGAGAACACTATGAGCTTCCGAGTTTCAAAAGTTTCTTGAAGTGAATTCAGT 329
|||
QY 461 GAGGAGAACATTTTTCATCTACTAAAGAGTAATTTGCTAAGAGCATCGCCCGAGCCCACT 520
|||

Db 330 GAGGAAACCTTGAGTCTCGGATGCGCTGAGGATTACAAGATCAATGCCCTGCC 389
QY 521 CAATCATCTAAAGCAAGCAATCATGAGAAATTCATTGAGATGATGCCCAAA 580
Db 390 AAGTGGCTGAGAGGCAAGCAATTTATGAAGATTCATTCAAACGGAGGCTCCTAA 449
QY 581 GAGGTATACATGATTTTCATACATAAGAAATGCTTAAGAGCATGCCCAAGCCACT 640
Db 450 GAGGTGAATATTGACCACTTCACTAAGACATCAATGAAGAACCCTGGTGGAACTTCC 509
QY 641 CTCACAGTTTGTATACGGCAAGCAGAGTGATCCAGCTCATGGACATGACAGATTAT 700
Db 510 CTGACACCTTTGACATGCCCAAGAAAGATCAATGCGCTGAGGAAAGATTCCTG 569
QY 701 AAACCTTTTGAATCTGAGACCTACTTACATTTGAT 738
Db 570 CCTCGTTTGTGCGCTGCTGAGTTTATCAGGAGTTAAT 607

RESULT 10

US-09-016-434-1091
; Sequence 1091, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1091:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1216372
US-09-016-434-1091

Query Match 11.9%; Score 139; DB 4; Length 800;
Best Local Similarity 56.6%; Pred. No. 6e-26;
Matches 278; Conservative 0; Mismatches 210; Indels 3; Gaps 1;
QY 251 AGAGCGAAAGAAAGGATAGACTAAGTCTTCTCTACAGAGCGCTGACTTCCATGGA 310

Db 140 AGTGCAAAAGATATGAACAATCGGCTAGGTTTCTCTGTCGAAAAATCTGATTCCTGTGAA 199
QY 311 GAGA---CTCAAGCCAGTAGATCTGCCCTCTCTGGCCCAAGAAACAAGAGTCTCTCTCGAA 367
Db 200 CACAATTTCTCCACAACAAGAGGACAAAGTGTTTATTGGCCAGAGAGTGAGCCCAAGAG 259
QY 368 GAAGCAGTGAATTTGGGCTGAATCATTTGACAAATTCCTCTCTCATAGAGATGAGTGGAT 427
Db 260 GAAGTCAAGAAATTTGGGCTGAATCACTGGAAACCTGATTAGTCATGAATGTGGGCTGGCA 319
QY 428 GCTTTTACCAGATTCTTAAACTGAATTCAGTGAGGAGAACTTGAATTTTGGGTCGCC 487
Db 320 GCTTTCAAGCTTTCTTGAAGTCTGAATATAGTAGGAGAGAAATTTGACTTCTGERTCAGC 379
QY 488 TGTGAAGACTTCAAGAAATCAAGAACTTCAACAAATCATCTTAAAGCAAGGCAATC 547
Db 380 TGTGAAGACTTCAAGAAATCAATCACTTAAACTAAGTCCCAAGGCCAAAGATC 439
QY 548 TATGAGAAATTCATTGAGATGATGCCCCCAAGAGGTTAACTGATTTTCATATAA 607
Db 440 TATAATGAATTCATCTCAGTCCAGGCAACCAAGAGGTTGAACCTGATTTCTTGCCACAGG 499
QY 608 GAAGTAATTGCTAAGAGCATCGCCAGCCCACTCTCCACAGTTTGTATACGGCACAAGC 657
Db 500 GAAGAGACAAGCCGGAACATGCTAGAGCCTTACAATAACCTGCTTTGATGAGGCCCAAG 559
QY 668 AGAGTGTACAGCTCATGGACATGACAGTTATAAAGCGTTTGTGAATCTGACACTAC 727
Db 560 AGATTTTCAACCTGATGAGAGAGGATCTTACCGCGCTTCTCAAGTCTCGATTTCTAT 619
QY 728 TTACATTTGAT 738
Db 620 CTTGATTTGCT 630

RESULT 11

US-09-566-921-111
; Sequence 111, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566, 921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 111
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 900146.4
US-09-566-921-111

Query Match 11.7%; Score 136; DB 4; Length 3208;
Best Local Similarity 60.6%; Pred. No. 5.8e-25;
Matches 223; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 371 GCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCATAGAGATGAGTGGATGCT 430
Db 321 GCCTGCGAGTGGCGTGATTCCTTGGACAAACTCTCGAGAACAACTATGACTTGCAGT 380
QY 431 TTTCACGATTTCTTAAACTGAATTCAGTGAGGAGAACTTGAATTTGGGTCGCTGT 490
Db 381 TTCAAAGTTTCTGAGTCTGAATTCAGTGAGGAAACCTTGAGTTCTGGATTGCTGT 440
QY 491 GAAGACTTCAAGAAATGCAAGGAACTCAACAAATCATCTTAAAGCAAGGCAATCTAT 550


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1398 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9299704
US-09-016-434-1290

Query Match      11.2%; Score 129.8; DB 4; Length 1398;
Best Local Similarity 60.2%; Pred. No. 1.6e-23;
Matches 234; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

QY 355 AGTCTCTCTCGAAGACGAGTGAATGGGTGAATCAATTTGACAAATTTGCTCTCTCATAG 414
Db 278 ACTTTCTGCTGCTGAAGTAAATGGAATGCTCAATCTCTGAAAAAATCTTTTGCCAAACA 337

QY 415 AGATGGAGTGTGATGCTTTTACCAGATTTCTTAAACATGAATTCAGTGCAGGAGACATTGA 474
Db 338 AACTGGTCAAAATGTCTTTGGAGTTTCTTAAAGTCTGAATTCAGTGCAGGAGAAATATTGA 397

QY 475 ATTTTGGGTGCGCTGTGAAGACATTTCAAGAAATTCAGATGATGCCCCCAAGAGGTTAACATTGA 534
Db 398 GTTCTGCTGCTGCTGAAGTAAATGGAATGCTCAATCTCTGAAAAAATCTTTTGCCAAACA 337

QY 415 AGATGGAGTGTGATGCTTTTACCAGATTTCTTAAACATGAATTCAGTGCAGGAGACATTGA 474
Db 338 AACTGGTCAAAATGTCTTTGGAGTTTCTTAAAGTCTGAATTCAGTGCAGGAGAAATATTGA 397

QY 475 ATTTTGGGTGCGCTGTGAAGACATTTCAAGAAATTCAGATGATGCCCCCAAGAGGTTAACATTGA 534
Db 398 GTTCTGCTGCTGCTGAAGTAAATGGAATGCTCAATCTCTGAAAAAATCTTTTGCCAAACA 337

QY 535 AGCAAAAGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTTAACATTGA 594
Db 455 AGCAGAGAGATATATAAGCAATTTGTGCAATTCAGATGCTGCTTAAACAATCAATATTGA 514

QY 595 TTTTCTACTAAAGAGTAATTTGCTTAAGAGCATGCGCCAGCCACTCTCCACAGTTTGA 654
Db 515 CTTCGGCACTCGAGATCTACAGCCAGAGATTAAGCACCACCCCGACGTTTGA 574

QY 655 TACGGCAAAAGCAGAGTGTACAGCTCATGGAACATGACAGTTTATAACGCTTTTGA 714
Db 575 TGAAGCAAAAGTCTATATATCTTTATGGAAGAGGACTCTTATCCAGGTTCTCTCAA 634

QY 715 ATCTGAGACCTACTTACATTTGATAGAAG 743
Db 635 ATCAGATATTCTTAATCTTCTAAATG 663

RESULT 14
US-09-702-705-322
; Sequence 322, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 322
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-322

Query Match      11.2%; Score 129.8; DB 4; Length 1398;
Best Local Similarity 60.2%; Pred. No. 1.6e-23;
Matches 234; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

QY 355 AGTCTCTCTCGAAGACGAGTGAATGGGTGAATCAATTTGACAAATTTGCTCTCTCATAG 414
Db 278 ACTTTCTGCTGCTGAAGTAAATGGAATGCTCAATCTCTGAAAAAATCTTTTGCCAAACA 337

QY 415 AGATGGAGTGTGATGCTTTTACCAGATTTCTTAAACATGAATTCAGTGCAGGAGACATTGA 474
Db 338 AACTGGTCAAAATGTCTTTGGAGTTTCTTAAAGTCTGAATTCAGTGCAGGAGAAATATTGA 397

QY 475 ATTTTGGGTGCGCTGTGAAGACATTTCAAGAAATTCAGATGATGCCCCCAAGAGGTTAACATTGA 534
Db 398 GTTCTGCTGCTGCTGAAGTAAATGGAATGCTCAATCTCTGAAAAAATCTTTTGCCAAACA 337

QY 535 AGCAAAAGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTTAACATTGA 594
Db 455 AGCAGAGAGATATATAAGCAATTTGTGCAATTCAGATGCTGCTTAAACAATCAATATTGA 514

QY 595 TTTTCTACTAAAGAGTAATTTGCTTAAGAGCATGCGCCAGCCACTCTCCACAGTTTGA 654
Db 515 CTTCGGCACTCGAGATCTACAGCCAGAGATTAAGCACCACCCCGACGTTTGA 574

QY 655 TACGGCAAAAGCAGAGTGTACAGCTCATGGAACATGACAGTTTATAACGCTTTTGA 714
Db 575 TGAAGCAAAAGTCTATATATCTTTATGGAAGAGGACTCTTATCCAGGTTCTCTCAA 634

QY 715 ATCTGAGACCTACTTACATTTGATAGAAG 743
Db 635 ATCAGATATTCTTAATCTTCTAAATG 663

RESULT 15
US-09-736-457-322
; Sequence 322, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, AiJun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 322
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-322

Query Match      11.2%; Score 129.8; DB 4; Length 1398;
Best Local Similarity 60.2%; Pred. No. 1.6e-23;
Matches 234; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

QY 355 AGTCTCTCTCGAAGACGAGTGAATGGGTGAATCAATTTGACAAATTTGCTCTCTCATAG 414
Db 278 ACTTTCTGCTGCTGAAGTAAATGGAATGCTCAATCTCTGAAAAAATCTTTTGCCAAACA 337

QY 415 AGATGGAGTGTGATGCTTTTACCAGATTTCTTAAACATGAATTCAGTGCAGGAGACATTGA 474
Db 338 AACTGGTCAAAATGTCTTTGGAGTTTCTTAAAGTCTGAATTCAGTGCAGGAGAAATATTGA 397

QY 475 ATTTTGGGTGCGCTGTGAAGACATTTCAAGAAATTCAGATGATGCCCCCAAGAGGTTAACATTGA 534
Db 398 GTTCTGCTGCTGCTGAAGTAAATGGAATGCTCAATCTCTGAAAAAATCTTTTGCCAAACA 337
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10518.000 Million cell updates/sec
(without alignments)

Result No.	Score	Query Match	Length	DB	ID	Description
1	1164	100.0	1164	9	US-09-894-749-3	Sequence 3, Appli
2	602.6	51.8	1884	17	US-10-115-635-133	Sequence 133, App
3	599.6	51.5	1840	13	US-10-258-371B-18	Sequence 18, App
4	599.6	51.5	214	13	US-10-258-371B-19	Sequence 19, App
5	591.2	2217	591	9	US-09-894-749-1	Sequence 1, Appli
6	560.6	48.2	848	9	US-09-867-550-847	Sequence 847, App
7	305.4	26.2	736	9	US-09-833-381-1010	Sequence 1010, Ap
8	192.2	15.5	1486	13	US-10-238-371B-6	Sequence 6, Appli
9	177.6	15.3	241	13	US-10-258-371B-11	Sequence 11, App
10	152.4	13.1	1345	13	US-10-342-487-839	Sequence 839, App
11	152.4	13.1	1345	13	US-10-172-118-839	Sequence 839, App
12	152.4	13.1	1345	16	US-10-305-720-1278	Sequence 1278, App
13	152.4	13.1	1345	17	US-10-641-643-1243	Sequence 1243, App
14	152.4	13.1	1364	9	US-09-925-300-567	Sequence 567, App

121 ACTGGGACAGATAATGGATATGTCAGTCTGTTCTCTCTCAATTAATATGTTGTAATC 180
 181 AAAAGAGAAAACCTTTTCAAACTAATCATGATGGGTGAGGAAAGAGAAACAAAGCATCGA 240
 181 AAAAGAGAAAACCTTTTCAAACTAATCATGATGGGTGAGGAAAGAGAAACAAAGCATCGA 240
 241 GGCCTCAATTCAGAGCGAAAGAAAAGGAATAGACTAAGTCTTCTCTACAGAGGCGCTCGA 300
 241 GGCCTCAATTCAGAGCGAAAGAAAAGGAATAGACTAAGTCTTCTCTACAGAGGCGCTCGA 300
 301 CTTCCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGCCCAAGAAACAAAGAGTCTC 360
 301 CTTCCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGCCCAAGAAACAAAGAGTCTC 360
 361 TCCCTGAAGAGCAGTGAATGGGCTGAAATCATTTGACAAATGCTCTCTCATAGAGATGG 420
 361 TCCCTGAAGAGCAGTGAATGGGCTGAAATCATTTGACAAATGCTCTCTCATAGAGATGG 420
 421 AGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGGAAACATTTGATTTTG 480
 421 AGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGGAAACATTTGATTTTG 480
 481 GGTGCGCTGTGAAGACTTCAAGAAATGCAAGAACTCAAGAAATCATCTTAAAGCAAA 540
 481 GGTGCGCTGTGAAGACTTCAAGAAATGCAAGAACTCAAGAAATCATCTTAAAGCAAA 540
 541 GGCATCTATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTTAAACATTTTCA 600
 541 GGCATCTATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTTAAACATTTTCA 600
 601 TACTAAGAGTAAATTCAGAGAGATGCGCCAGCGCCACTCTCCACAGTTTGTAGCGC 660
 601 TACTAAGAGTAAATTCAGAGAGATGCGCCAGCGCCACTCTCCACAGTTTGTAGCGC 660
 661 ACAAGCAGAGTGTACAGCTCATGAAATGACAGAGTATTAACGCTTTTGAATCTGA 720
 661 ACAAGCAGAGTGTACAGCTCATGAAATGACAGAGTATTAACGCTTTTGAATCTGA 720
 721 GACCTACTTACATTTGATAGAGAGAGCCTCAGAGACCAACAAACCTTAGAGAGCATC 780
 721 GACCTACTTACATTTGATAGAGAGAGCCTCAGAGACCAACAAACCTTAGAGAGCATC 780
 781 AGCATCATTTACTTACAATGATTTCCAGATGTAAGTCAAGTGTGCTTGGTTATG 840
 781 AGCATCATTTACTTACAATGATTTCCAGATGTAAGTCAAGTGTGCTTGGTTATG 840
 841 AGTAAAGTCAITTTGCTCTTTTATGATGTATGTATATCTAAATATATATACTAATA 900
 841 AGTAAAGTCAITTTGCTCTTTTATGATGTATGTATATCTAAATATATATACTAATA 900
 901 CTAATGTGACTCTTAAATATAGCTTGTGATAGAGAGATGATTTCAATTTTAAAT 960
 901 CTAATGTGACTCTTAAATATAGCTTGTGATAGAGAGATGATTTCAATTTTAAAT 960
 961 ACACCATGCAATATATTAATGTAAGAACTTTTATATATATATACTAAATATATC 1020
 961 ACACCATGCAATATATTAATGTAAGAACTTTTATATATATATACTAAATATATC 1020
 1021 ATCTATCTCCGAAATATTTTATGAAATCTATCTGATATCTTCTTAAATATTTCT 1080
 1021 ATCTATCTCCGAAATATTTTATGAAATCTATCTGATATCTTCTTAAATATTTCT 1080
 1081 TATTTCTACAATAACAGTCAAGTGAAGAGAGCTTTGAAGCGAATTCAGACACCTGGC 1140
 1081 TATTTCTACAATAACAGTCAAGTGAAGAGAGCTTTGAAGCGAATTCAGACACCTGGC 1140
 1141 GCGGTACTAGTGGATCCGAGTCT 1164
 1141 GCGGTACTAGTGGATCCGAGTCT 1164

US-10-115-635-133
 ; Sequence 133, Application US/10115635
 ; Publication No. US20040137434A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: Novel Nucleic Acids and
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 797CON
 ; CURRENT APPLICATION NUMBER: US/10/115,635
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: 09/714,936
 ; PRIOR FILING DATE: 2000-11-17
 ; NUMBER OF SEQ ID NOS: 362
 ; SOFTWARE: pt_FL_genes Version 2.0
 ; SEQ ID NO 133
 ; LENGTH: 1884
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (157)..(864)
 US-10-115-635-133
 Query Match 51.8%; Score 602.6; DB 17; Length 1884;
 Best Local Similarity 75.3%; Pred. No. 3.7e-120;
 Matches 817; Conservative 0; Mismatches 234; Indels 34; Gaps 4;
 QY 1 TTTTGTGAGAAAACTCTGAGGAAAGATTCCGGATAGCGCTTTATTC-AGGATGTTTTCC 59
 DB 25 TTTCTTTTGTAAACATTACTGTAGAGTTGTGATTAACCTTTTATTTACTACTATGATATG 84
 QY 60 TATGAATAGCATTCATCTGTGGAGAGAGAGGACTAAGAAATCTGACATCTGTGGT 119
 DB 85 TATGGAATAGTATTAATAAATGAATAGGAGGATGTAATAAATAGACATCTCTTCAT 144
 QY 120 CACTGGGACAGATATGGATATGTCAGTCTGTTTCTCTCAATTAATATATGTGTAAT 179
 DB 145 T--TTAGAGAGAGATGGAAACAAACATTTGCTTTTCTCTCAATAAATAATGTGTAAT 202
 QY 180 CAAAAGAGAAAACTTTTTTCAAACTAATGATGGGTGAGGAAAGAAAGAAACAAAGCATCG 239
 DB 203 CAAAAGAAAACTTTTTTCAAGTTAATACATCGTTTCAAGAAAAAGAAACAAAGCAAAG 262
 QY 240 AGGCCAAATCAGAGCGAAAGAAAGGAATAGACTTCTCTCTACAGAGCGCTG 299
 DB 263 AAGCCAAATCAGAGCTGAGGAAAAAGAAATAGACTTCTCTCTGCGAAACCTG 322
 QY 300 ACTTCCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAACAAAGAGTCT 359
 DB 323 AGTTTCATGAAGACACCCGCTCCAGTAGATCTGGCCACTTGGCCAAAGAAACAAAGAGTCT 382
 QY 360 CTCCTGAAGAGCAGTGAATGGGCTGATCATTTTGAACAAATGCTCTCTCATAGAGATG 419
 DB 383 CCCCTGAAGAGGAGTGAATGGGGTGAATCATTTTGAACAAACCTGCTTCCCATAGAGATG 442
 QY 420 GAGTGGATGCTTTTACAGATTTCTTAAACTGAAATTCAGTGAAGGAAACATTTGAATTTT 479
 DB 443 GACTAGAGGCTTTTACAGATTTCTTAAACTGAAATTCAGTGAAGGAAATATTTGAATTTT 502
 QY 480 GGTGCGCTGTGAAGACTTCAAGAAATGCAAGAACTCAAGAAATCATCTTAAAGCAAA 539
 DB 503 GGATAGCCTGTGAAGATTTCAAGAAAAAGCAAGGAGCTCAACAAATTCACCTTTAAAGCAA 562

QY 540 AGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCAAAGAGGTTAAACATTCATTTTC 599
DB 563 AAGCAATATATGAGAAATTTATACAGACTGATGCCCCAAAGAGGTTAAACATTCATTTTC 622
QY 600 ATACTAAAGAAAGTAAATTCCTAAGAGCATCGCCAGCCCACTCTCCACAGTTTTCATACGG 659
DB 623 ACACAAAAGAAAGTCAATTAACAAACAGCATCACTCAACCTACCCTCCACAGTTTTCATGCTG 682
QY 660 CACAAAGCAGAGTGTACAGCATCTGGAACATGACAGTTATATAAAGCTTTTGAATCTG 719
DB 683 CACAAGCAGAGTGTATCAGCTCATGGAACAGACAGTTATACAGTTTTCGTAATCTG 742
QY 720 AGACCTACTTACATTTGATAGAAGAACACCTCAGAGACCAACAAACCTTAGGAGAGCAT 779
DB 743 ACATCTATTTAGACTTGTAGGAAGAACCTCAGAGACCAACAAATCTTAGGAGAGCAT 802
QY 780 CACGATCATTTTACATTAATGATTTCCAAAGATGTAAGTCAAGTGTGCCATTTGGTTAT 839
DB 803 CACGCTCATTTTACCTGCAATGAATTCCAAGATGTACAAATCAGATGTGCCATTTGGTTAT 862
QY 840 CAGTAAAGAGTCAATTTGCTCTCTTTTGAATGATGTGTATATCTAAATATATACATAAT 899
DB 863 AAGAAATTTGATTTGCTCATTTTATGACAAACTTATATATC----- 906
QY 900 ACTAATGTGTACTTCTTAAATATATAGTTGTGTATAAGAGAGATGATTTCAATTTT----- 954
DB 907 -----TGCTTCAACATATGCAATGTTTATGTTAAGATTTGGTCCCATCTCTTAA 957
QY 955 -TAAATACACCATGCAATATCAATTAATAAGTAAGAACTTTTATATATATATAATA 1013
DB 958 CTGAATATGTATGTGAATTTTAAATGTAAACAAACCTTTCTGCTTAACAA 1017
QY 1014 ATTCATCATCTATCTTCGAAATATTTTATGAAATCTATCTGATATTTCTATTTCTAATAA 1073
DB 1018 ATACATACAGTATCTGCCAGTATATCTGTAAACCTTCTATTTGATGTCAATTCATTTA 1077
QY 1074 AATTC 1078
DB 1078 TAATC 1082

RESULT 3

US-10-258-371B-18
; Sequence 18, Application US/10258371B
; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Alison
; APPLICANT: MURRAY, David L
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
; TITLE OF INVENTION: RGS18, AND USES THEREOF
; FILE REFERENCE: A3656 US PCT
; CURRENT APPLICATION NUMBER: US/10/258,371B
; CURRENT FILING DATE: 2003-06-04
; PRIOR FILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-08-02
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; TYPE: DNA
; LENGTH: 1840
; ORGANISM: Homo sapiens
US-10-258-371B-18

Query Match 51.5%; Score 599.6; DB 13; Length 1840;
Best Local Similarity 75.2%; Pred. No. 1.6e-119;
Matches 814; Conservative 0; Mismatches 234; Indels 34; Gaps 4;
QY 4 TTGTAAGAAATCTGAGAAAGATTCGGGATAGCGTTTATTC-AGGATGTTTCTCTAT 62
DB 34 TTTTGTGAAACATTAATCTGTAAGAGTTGTGATAACTTTTATTTATCTATGATATGAT 93

QY 63 GAATAGCATTCATCTCTGTGGAGAGAGGACTAAGGAAATCTGACATCTGTGTGTCAC 122
DB 94 GGAATAGTATTATAAATGAACCTAGGAAGGATGTAATAAATTAGACATCTCTTCATT-- 151
QY 123 TGGGACAGAAATATGGATATGTCTACTGGTTTTCTCTCAATTTAAATATGTGTGAATCAA 182
DB 152 TTAGAGAGAAGATGGAACCAACATTCCTTTCTCTCAATTAATATGTGTGTGAATCAA 211
QY 183 AAGAGAAATCTTTTTCAAACTAATCGATGGGTGAGGAAAGAGAAACAAGCATCGAG 242
DB 212 AAGAAATAACTTTTTCAGAGTTAATACATGGTTTCAGAAAGAGAAACAAGCAAGAAG 271
QY 243 CCAAAATCAGAGCAAGAAAGAAAGCAATAGACTAAGTCTTCTCTACAGAGCCCTGACT 302
DB 272 CCAAAATCAGAGCTAAGGAAAGAAATAGACTAAGTCTTCTGTGCAAGAACCTGAGT 331
QY 303 TCATGAGAGAGCTAAGGAGAGTAGATCTGCGCTCTTGGCCAAAGAAACAAGAGTCTCTC 362
DB 332 TTCATGAAGACACCCGCTCAGTAGATCTGGGCACTTGGCCAAAGAAACAAGAGTCTCC 391
QY 363 CTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTCGTTCCCATAGAGATGGAC 422
DB 392 CTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTCGTTCCCATAGAGATGGAC 451
QY 423 TGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGGAGAAACATTTGAATTTGG 482
DB 452 TAGAGGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGGAGAAATATTTGAATTTGG 511
QY 483 TCGCTGTGAGAGATTCAGAAATGCAAGAACTCAAGAACTCAACAAATCATCTTAAAGCAAG 542
DB 512 TAGCCTGTGAAGATTTCAAGAAAGCAGGAGCTCAACAAATTCACCTTAAAGCAAGAA 571
QY 543 CAATCTATCAGAAATTCATTTCAGATGATGCCCCCAAGAGGTTAAACATTTGATTTTCA 602
DB 572 CAATATATGAGAAATTTATACAGCTGATGCCCAAGAGGTTAAACCTCGATTTTCA 631
QY 603 CTAAGAGATGATGCTAAGAGATCGCCGAGCCCACTCTCCACAGTTTGTATACGGCAC 662
DB 632 CAAAGAAAGTCATTACAAACAGCATCACTCAACCTACCCCTCCACAGTTTGTATGCTGC 691
QY 663 AAAGCAGAGTGTAACAGCTCATGGAACATGACAGTTTATAAAGCTTTTGAATTTGAGA 722
DB 692 AAAGCAGAGTGATACAGCTCATGGAACAGAGATGATATACAGTTTCTGAAATCTGACA 751
QY 723 CCTACTTACATTTGATAGAAGAGACCTCAGAGACCAACAAACCTTAGGAGACGATCAC 782
DB 752 TCTATTTAGACTTGTATGGAAGAGAGACCTCAGAGACCAACAAATCTTAGGAGACGATCAC 811
QY 783 GATCATTCTACTTACATGATTTCCAGATGTAAGTCAGATGTCGATTTGGTTATGAG 842
DB 812 GCTCATTTACCTGCAATGAATTTCCAAGATGTACAAATCAGATGTTGCCATTTGGTTATAA 871
QY 843 TAAAGTCAATTTGCTCTCTTTGATAGTGTATGTATATCTTAAATATATATACTAATACT 902
DB 872 GAAATTTGATTTTGTCTCATTTTATGACAACTTATACATC----- 912
QY 903 AATGCTACTTCTTAAATATAGCTTGTGTATAGAAGAGATGATTTTCATTTT-----TA 956
DB 913 -----TGCTTCTAACATATGCGATGTTTATGTATAGATTTGGTCCCATCTTTAAACATG 966
QY 957 AAATACCATGCAATATATATAATTAAGAACTTTTATATATATACTATAAATAAT 1016
DB 967 AATATGTCATGTGAATTTATTTAAATGTAAACAAACAACTTCTGCTAACAAATA 1026
QY 1017 CATCATCTATCTCCGAAATATTTATGAAATCTATCTGATATTCATTTCTATTAATAAAT 1076
DB 1027 CATACAGTATCTGCCAGTATATCTGTAAAAACCTTCTATTTGATGTCAATTCATTTATAA 1086
QY 1077 TC 1078
DB 1087 TC 1088

RESULT 4
US-10-258-371B-19
; Sequence 19, Application US/10258371B
; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Alison
; APPLICANT: MURRAY, David L
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
; TITLE OF INVENTION: RGS18, AND USES THEREOF
; FILE REFERENCE: A3656 US PCT
; CURRENT APPLICATION NUMBER: US/10/258,371B
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: GB001883.334
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/200,786
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 2144
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-258-371B-19

Query Match 51.5%; Score 599.6; DB 13; Length 2144;
Best Local Similarity 75.2%; Pred. No. 1.8e-119;
Matches 814; Conservative 0; Mismatches 234; Indels 34; Gaps 4;
QY 4 TTGTAAAGAAATCTGACGAGAGATTCGGGATAGCGCTTTATTC-AGGATGTTTTCTCTAT 62
DB 34 TTTTGTGAAACATTACTGTAGAGTGTGTGAATCTTTTATTTCTACTATATATGAT 93
QY 63 GAAATAGCATTCATCTGTGGGAGAGAGAGGACTAAGGAAATCTGACATCTGTGGTGCAC 122
DB 94 GGAATAGTATTAAATAATGAAGTACTAGGAGAGGATGTAATAATTAGACATCTCTCAIT-- 151
QY 123 TGGGACAGAAATATGATATGTCACCTGTTTCTCTCTCAATTAATATGTGTAATCAA 182
DB 152 TTAGAGAGAGATGGAAACAAATGCTTTCTTTCTTCAAAATAATATGTGTAATCAA 211
QY 183 AAGACAAATCTTTTCAAACTAATGTCAGGTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 242
DB 212 AAGAAACATTTTCAAGTTAATACATGTTTCAAGAAAGAGAGAGAGAGAGAGAGAGAG 271
QY 243 CCAAAATCAGAGCGAG 302
DB 272 CCAAAATCAGAGCTAAGGAG 331
QY 303 TCCATGGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAGAGAGAGAGAGAG 362
DB 332 TTCATGAGACACCCGCTCCAGTAGATCTGGCAGCTTGGCCAAAGAGAGAGAGAGAGAG 391
QY 363 CTGAAG 422
DB 392 CTGAAG 451
QY 423 TGGATGCTTTTACAGAGATTTCTTAAACTGAATTCAGTGGAGAGAGAGAGAGAGAGAG 482
DB 452 TAGAGGCTTTTACAGAGATTTCTTAAACTGAATTCAGTGGAGAGAGAGAGAGAGAGAG 511
QY 483 TCGCCTGTGAAGACTTCAAGAAATGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
DB 512 TAGCCTGTGAGATTTCAAGAAAGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571
QY 543 CAATCTGAG 602
DB 572 CAATATGAG 631
QY 603 CTAAG 662
DB 632 CAAAG 691

QY 663 AAAGCAGAGTGTACCAGCTCATGGAAACATGACAGTTATAAAACGCTTTTGGAAATCTGAGA 722
DB 692 AAAGCAGAGTGTATCAGCTCATGGAAACAAAGACAGTTATACACGTTTCTGAAATCTGACA 751
QY 723 CCTACTTACATTTGTAG 782
DB 752 TCTATTTAGACTTGTAG 811
QY 783 GATCATTTTACTTACAAATGATTTCCAGAGATGTAAGATCGAGATGTTGCCATTTGGTTATGAG 842
DB 812 GCTCATTTTACCTGCAATGAATTTCCAGAGTACAAATCAGATGTTGCCATTTGGTTATGAA 871
QY 843 TAAAGTCAATTTGCTCTCTTTTGTAGTGTATGCTATATCTAAATAATATATATCTAAATCT 902
DB 872 GAAATTTGATTTTGTCTCAATTTTATGACAAACTTTATACATC----- 912
QY 903 AATGTGACTTCTAAATATAGCTTGTGTATAAGAGAGAGATGATTTTCATTTT-----TA 956
DB 913 -----TGCTTCTACATATCGCATGTTTATGTTAAGATTTGGTCCCATCTTTTAAACTG 966
QY 957 AAATACACCATGCAAAATACATATTAATGTAAGACCTTTTATATATATATATATATATATAT 1016
DB 967 AAATATGTCATGTGAAATTAATTTTAAATAATGTAAGAAACAAATCTTCTGCTAACAAATA 1026
QY 1017 CATCATCTATCTCCGAAATATTTTATGAAATCTATCTGATATTTCTTCTTAATAAAT 1076
DB 1027 CATACAGTATCTGCCAGTATATTTCTGTAACCTTCTAATTTGATGATCTATCCATTTATA 1086
QY 1077 TC 1078
DB 1087 TC 1088

RESULT 5
US-09-894-749-1
; Sequence 1, Application US/09894749
; Patent No. US20020081683A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, David
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/894,749
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/244,314
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2217
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)...(867)
US-09-894-749-1

Query Match 51.2%; Score 596; DB 9; Length 2217;
Best Local Similarity 75.8%; Pred. No. 1.1e-118;
Matches 791; Conservative 0; Mismatches 220; Indels 33; Gaps 3;
QY 41 TTTATTTCAGAGTGTTCCTATGAAATAGCATTCATCTGTGGAGAGAGAGAGAGAGAGAG 100
DB 69 TTATTCTACTATGATATGATATGTAATAGTATTAATAATGAAATAGGAGAGAGATTAAT 128
QY 101 AAATCTGACATCTGTTGGTCACTGGGACAGATATGATATCTCACTGGTTTCTTCTCTCT 160
DB 129 AAATAGACATCTCTTCAT--TTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
QY 161 CAATTAATATGTTGTAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 220
DB 187 CAAATTAATATGTTGTAATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246

Qy	221	AAAGAGAAAC	AGAGCATCGAGCCAAAATCAGACCGGAAAGAAAAGGAATAGACTAAGT	280
Db	247	AAAGAGAAAC	AGAGCAAGGAGCCAAAATCAGACCTAAGGAAAGAAAAGAAATAGACTAAGT	306
Qy	281	CTTCTCCT	CACAGAGGCTGACTTCATCGGAGAGACTCAAGCCAGTAGATCTGCGCTCTTG	340
Db	307	CTTCTGTG	CGAAGACCTGAGTTTCATGAAGACACCCGCTCCAGTAGATCTGGGCACTTG	366
Qy	341	GCCAAAGAA	ACAAAGAGTCTCTCTGAAGACAGCAGTGAAATGGGCTGAATCATTTGACAAA	400
Db	367	GCCAAAGAA	ACAAAGAGTCTCCCTCGAAGAGCAGTGAAATGGGCTGAATCATTTGACAAA	426
Qy	401	TTGCTCTC	TATAGAGATGGAGTGATGCTTTTACCAGATTCTTTAAACTGAAATTCAGT	460
Db	427	CTGCTTTCC	ATAGAGATGGACTAGAGGCTTTTACCAGATTCTTTAAACTGAAATTCAGT	486
Qy	461	GAGGAGAAC	ATTTGAATTTTGGGTGCGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAA	520
Db	487	GAGAAATAT	TGAAATTTGGATAGCCCTGTGAAGATTTCAAGAAAGCAAGGGACCTCAA	546
Qy	521	CAAAATCAT	CTTAAAGCAAGGCAATCTATCAGAAATTCATTGAGAAATGATGCCCCCAA	580
Db	547	CAAAATCAC	CTTAAAGCAAAAGCAATATATGAGAAATTTATACAGACTGATGCCCCCAA	606
Qy	581	GAGGTTAA	CAATTTGATTTTCATACTAAAGAACTAATTCCTAAGAGCATCGCCAGGCCACT	640
Db	607	GAGGTTAAC	CTTGAATTTTCACACAAAGAACTCATTACAAACAGATCACTCAACCTACC	666
Qy	641	CTCCACAG	TTTTGATACGGCACAAAGCAGAGTGATCCAGCTCATGGAACATGACAGTTAT	700
Db	667	CTCCACAG	TTTTGATGCTGCAAAAGCAGAGTGATCAGCTCATGGAACAAAGACAGTTAT	726
Qy	701	AAACGCTT	TTCGAAATCTGAGACCTACTTCATTTGATGAAGAAAGAGACCTCAGAGACCA	760
Db	727	ACAGTTTCT	GAAATCTGACATCTATTTAGACTTTGATGAAGAAAGACCTCAGAGACCA	786
Qy	761	ACAAACCT	TAGAGACGATCAGATCAATTTACTTTCAATGATTTCCAAGATGTAAGTCA	820
Db	787	ACAAATCT	TAGAGACGATCAGCTCATTTACCTGCAATGAATTTCCAAGATGTACAATCA	846
Qy	821	GATGTTGC	CAATTTGATAGTAAAGTCAATTTGCTCTCTTTTGATAGTGTATGTAT	880
Db	847	GATGTTGC	CAATTTGTTTAAAGAAATTTGAATTTGCTCAATTTTATGACAACTTATAC	906
Qy	881	ATCTAAAT	TATATACTAATACTAATGTGTACTTCTAAATATATAGCTTTGTGTATAAGA	940
Db	907	ATC-----	-----TGCTTCTAACAATCGCATGTTTATGTTAAGA	941
Qy	941	GATGATTT	CAATTTT-----TAAATACACATGCAATACATTTAAATGTAGAGACTT	994
Db	942	TTTGGTCC	CAATCTTTAAACTGAAATATGTCAATGAAATTTATTTTAAAAATGTAAAA	1001
Qy	995	TTTATATAT	ACTAAAAAATTCATCTATCTTCCGAAATATTTTATGAAAAATCTATC	1051
Db	1002	AAAACTTCT	GTACAAATACATACAGTATCTGCGAGTATATTTCTGTAAACCTTCTA	1061
Qy	1055	TGATATCT	TAATTAATAATTC	1078
Db	1062	TTTGATGT	CAATTCATTTATAATC	1085

RESULT 6

```

; RESULT 6
; US-09-867-550-847
; Sequence 847, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby

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Query Match      15.3%; Score 177.6; DB 13; Length 241;
Best Local Similarity 83.8%; Pred. No. 1.3e-28;
Matches 201; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 461 GAGGAGAACATTGAATTTTGGCTGCCCTGTGAAGACTTCAAGAAATGCAAGAACCTCAA 520
DB 1 GAGGAAATCTGGAGTTCTGGATACCTGTGAAGATTTCAAGAAAGCAAGGGACCTCAA 60
QY 521 CAATCATCTTAAAGCAAGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCAAA 580
DB 61 CAATTCACCTTAAAGCAAGAAATATATAGAAATTTATACAGACTGATGCCCCAAA 120
QY 581 GAGGTAAACATTGATTTTCACTACTAAAGAAATGTAAGAGCATGCCCCAGCCACT 640
DB 121 GAGGTAAACCTTGAATTTTCAACAAAGAAAGTCAATCAACAGCATCACTCAACCTACC 180
QY 641 CTCACAGTTTGTATACGGCAAGACAGAGTGTACAGCTCATGGAAATGACAGATTAT 700
DB 181 CTCACAGTTTGTATACGGCAAGACAGAGTGTATACAGCTCATGGAAAGACAGACTAT 240

RESULT 10
US-10-342-887-839
; Sequence 839, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter S.
; APPLICANT: He, Yudong
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Mao, Mao
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 839
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-839

Query Match      13.1%; Score 152.4; DB 13; Length 1345;
Best Local Similarity 62.7%; Pred. No. 8.7e-23;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 359 TCTCTGAGAGAGTGAATGGCTGAATCAATTTGACAAATTTGCTCTCATAGAGAT 418
DB 249 TCTCTGAGGAGCAGCTGTGTGTCAGAGCAATTTGACGAGCTGTAGCCAGCAATAT 308
QY 419 GGAGTGGATGCTTTTACAGATTTCTTAAACTGAATTCAGTGGAGGAAACATTTGAATTT 478
DB 309 GGTCTTGCTGATTCAGGCTTTTAAAGTCGGATTTCTGTGAAGAAATATTTGAATTC 368
QY 479 TGGTGGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTTAAAGCA 538
DB 369 TGCTGGCTGTGAAGACTTCAAAAAACCAATCAACCCCAAGCTGTCTTCAAGCA 428
QY 539 AAGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCAAAGAGTTTAAATGATTTT 598
DB 369 TGGTGGCTGTGAAGACTTCAAAAAACCAATCAACCCCAAGCTGTCTTCAAGCA 428
QY 539 AAGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCAAAGAGTTTAAATGATTTT 598
DB 429 AGGAAATATATATCTGACTTTCATGAAAGGAGCTTCCAAAGAGATTAACATGATTTT 489
QY 599 CATACTAAAGAAATTAATGCTTAAGAGCATGCCCCAGCCACTCTCCACAGTTTGTATACG 658

Query Match      13.1%; Score 152.4; DB 13; Length 1345;
Best Local Similarity 62.7%; Pred. No. 8.7e-23;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 359 TCTCTGAGAGAGTGAATGGCTGAATCAATTTGACAAATTTGCTCTCATAGAGAT 418
DB 249 TCTCTGAGGAGCAGCTGTGTGTCAGAGCAATTTGACGAGCTGTAGCCAGCAATAT 308
QY 419 GGAGTGGATGCTTTTACAGATTTCTTAAACTGAATTCAGTGGAGGAAACATTTGAATTT 478
DB 309 GGTCTTGCTGATTCAGGCTTTTAAAGTCGGATTTCTGTGAAGAAATATTTGAATTC 368
QY 479 TGGTGGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTTAAAGCA 538
DB 369 TGCTGGCTGTGAAGACTTCAAAAAACCAATCAACCCCAAGCTGTCTTCAAGCA 428
QY 539 AAGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCAAAGAGTTTAAATGATTTT 598
DB 429 AGGAAATATATATCTGACTTTCATGAAAGGAGCTTCCAAAGAGATTAACATGATTTT 489
QY 599 CATACTAAAGAAATTAATGCTTAAGAGCATGCCCCAGCCACTCTCCACAGTTTGTATACG 658
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DB 489 CAAACCAAACACTCTGATTTGCCAGAAATATACAGAAAGCTTCAAGTGGCTGCTTTTCAACT 548
QY 659 GCACAAAGCAGAGTGTACCAAGCTCATGGAAACATGACAGTTATATAACGCTTTTGTAAATCT 718
DB 549 GCCCAGAAAAGGGTATACAGCTTGATGGAGAACAACTCTTATCTCTGTTCTTTGGAGTCA 608
QY 719 GAGACCTACTTACATTTG 736
DB 609 GAATCTTACCAGGACTTG 626

RESULT 11
US-10-172-118-839
; Sequence 839, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 839
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_002923
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-839

Query Match      13.1%; Score 152.4; DB 13; Length 1345;
Best Local Similarity 62.7%; Pred. No. 8.7e-23;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 359 TCTCTGAGAGAGTGAATGGCTGAATCAATTTGACAAATTTGCTCTCATAGAGAT 418
DB 249 TCTCTGAGGAGCAGCTGTGTGTCAGAGCAATTTGACGAGCTGTAGCCAGCAATAT 308
QY 419 GGAGTGGATGCTTTTACAGATTTCTTAAACTGAATTCAGTGGAGGAAACATTTGAATTT 478
DB 309 GGTCTTGCTGATTCAGGCTTTTAAAGTCGGATTTCTGTGAAGAAATATTTGAATTC 368
QY 479 TGGTGGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTTAAAGCA 538
DB 369 TGCTGGCTGTGAAGACTTCAAAAAACCAATCAACCCCAAGCTGTCTTCAAGCA 428
QY 539 AAGGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCAAAGAGTTTAAATGATTTT 598
DB 429 AGGAAATATATATCTGACTTTCATGAAAGGAGCTTCCAAAGAGATTAACATGATTTT 488
QY 599 CATACTAAAGAAATTAATGCTTAAGAGCATGCCCCAGCCACTCTCCACAGTTTGTATACG 658
DB 489 CAAACCAAACACTCTGATTTGCCAGAAATATACAGAAAGCTTCAAGTGGCTGCTTTTCAACT 548
QY 659 GCACAAAGCAGAGTGTACCAAGCTCATGGAAACATGACAGTTATATAACGCTTTTGTAAATCT 718
DB 549 GCCCAGAAAAGGGTATACAGCTTGATGGAGAACAACTCTTATCTCTGTTCTTTGGAGTCA 608
QY 719 GAGACCTACTTACATTTG 736
DB 609 GAATCTTACCAGGACTTG 626
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RESULT 12
 US-10-305-720-1278
 ; Sequence 1278, Application US/10305720
 ; Publication No. US20040010136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
 ; FILE REFERENCE: PA-0002-1 CON
 ; CURRENT APPLICATION NUMBER: US/10/305,720
 ; CURRENT FILING DATE: 2002-11-26
 ; PRIOR APPLICATION NUMBER: 09/016,434
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 1490
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1278
 ; LENGTH: 1345
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: GenBank ID No. US20040010136A1 g292054
 ; US-10-305-720-1278

Query Match 13.1%; Score 152.4; DB 16; Length 1345;
 Best Local Similarity 62.7%; Pred. No. 8.7e-23;
 Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY	359	TCCTCTGAAGACGAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCATAGAGAT	418
DB	249	TCTCTGAGGAGCAGCTGGTTCAGAGCATTTGACGAGTCTAGCCAGCAATAT	308
QY	419	GGAGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGGAGAACTTGAATTT	478
DB	309	GGTCTTGTGCTTTCAGGCTTTTAAAGTCGGAATTCCTGTGAAGAAATATTGAATTC	368
QY	479	TGGTGGCTGTGAGACTTCAGAAATGCAAGGAACTTCACAAATCATCTTAAAGCA	538
DB	369	TGGTGGCTGTGAGACTTCAGAAATGCAAGGAACTTCACAAATCATCTTAAAGCA	428
QY	539	AAGGCAATCTATGAGAAATTCATTTCAGATGATGCCCCCAAGAGGTTTAACTTGAATTT	598
DB	429	AGGAAATATATCTGACTTCATAGAAAGGAACTTCACAAATCATCTTAAAGCA	488
QY	599	CATCTAAGAGAGTAAATTCCTAAGAGATCGCCGAGCCACTCCACAGTTTTCATAG	658
DB	489	CAAAACCAAACTCTGATTCGCCAGATATACAAAGAGCTACAGTGGCTGCTTACAACT	548
QY	659	GCACAAAGCAGAGTGTACCAGCTCATGGAACATGACAGTTTAAAGCTTTTGAATCT	718
DB	549	GCCGAAAGGATATACAGCTTGTAGGAGAACAACTCTTATCTGTTCTTGAGTCA	608
QY	719	GAGACTTACTTACATTTG 736	
DB	609	GAATCTACAGGACTTG 626	

RESULT 13
 US-10-641-643-1243
 ; Sequence 1243, Application US/10641643
 ; Publication No. US20040077003A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; Jeffrey J. Seilhamer
 ; Susan G. Stuart
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA

COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/641,643
 FILING DATE: 14-Aug-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1243:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1345 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g292054
 SEQUENCE DESCRIPTION: SEQ ID NO: 1243 :
 US-10-641-643-1243

Query Match 13.1%; Score 152.4; DB 17; Length 1345;
 Best Local Similarity 62.7%; Pred. No. 8.7e-23;
 Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY	359	TCTCTGAAGACGAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCATAGAGAT	418
DB	249	TCTCTGAGGAGCAGCTGGTTCAGAGCATTTGACGAGTCTAGCCAGCAATAT	308
QY	419	GGAGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGGAGAACTTGAATTT	478
DB	309	GGTCTTGTGCTTTCAGGCTTTTAAAGTCGGAATTCCTGTGAAGAAATATTGAATTC	368
QY	479	TGGTGGCTGTGAGACTTCAGAAATGCAAGGAACTTCACAAATCATCTTAAAGCA	538
DB	369	TGGTGGCTGTGAGACTTCAGAAATGCAAGGAACTTCACAAATCATCTTAAAGCA	428
QY	539	AAGGCAATCTATGAGAAATTCATTTCAGATGATGCCCCCAAGAGGTTTAACTTGAATTT	598
DB	429	AGGAAATATATCTGACTTCATAGAAAGGAACTTCACAAATCATCTTAAAGCA	488
QY	599	CATCTAAGAGAGTAAATTCCTAAGAGATCGCCGAGCCACTTCACAGTTTTCATAG	658
DB	489	CAAAACCAAACTCTGATTCGCCAGATATACAAAGAGCTACAGTGGCTGCTTACAACT	548
QY	659	GCACAAAGCAGAGTGTACCAGCTCATGGAACATGACAGTTTAAAGCTTTTGAATCT	718
DB	549	GCCGAAAGGATATACAGCTTGTAGGAGAACAACTCTTATCTGTTCTTGAGTCA	608
QY	719	GAGACTTACTTACATTTG 736	
DB	609	GAATCTACAGGACTTG 626	

RESULT 14
 US-09-925-300-567
 ; Sequence 567, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben

;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

;; FILE REFERENCE: PA101

;; CURRENT APPLICATION NUMBER: US/09/925,300

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: PCT/US00/05988

;; PRIOR FILING DATE: 2000-03-08

;; PRIOR APPLICATION NUMBER: 60/124,270

;; PRIOR FILING DATE: 1999-03-12

;; NUMBER OF SEQ ID NOS: 1890

;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 567

;; LENGTH: 1364

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: (1362)

;; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-300-567

Query Match 13.1%; Score 152.4; DB 9; Length 1364;
Best Local Similarity 62.7%; Pred. No. 8.8e-23;
Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
Qy 359 TCTCTGAAGAGCAGTGAATGGCTGCAATCATTTGACAAATTTGCTCTCTCATAGAGAT 418
Db 246 TCTCTGAAGAGCAGCAGCTGTGTGTCAGAGCAATTTGACGAGTGTCTAGCCAGCAATAT 305
Qy 419 GGAGTGGATGTTTACAGATTTCTTTAAACTGAATTCAGTGGAGGAGCAATTTGAATTT 478
Db 306 GGTCTTGTCATTCAGGGCTTTTAAAGTCGGAATTTCTGTGAAGAAATATTTGAATTC 365
Qy 479 TGGCTGGCTGTGAAGCTTCAGAAATGCAAGAACTCAGCAATCATCTCAATCAAAAGCA 538
Db 366 TGGCTGGCTGTGAAGCTTCAGAAATGCAAGAACTCAGCAATCATCTCAATCAAAAGCA 425
Qy 539 AAGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTTTAACTTGAATTT 598
Db 426 AGGAAATATATATCTGACTTCATAGAAAGGAAGCTCCAAAGAGATATAACATAGATTT 485
Qy 599 CATACTAAGAAAGTAAATGCTTAAGAGCATGCCCGAGCCACTCTCCACAGTTTGTATCG 658
Db 486 CAACCAAAACTCTGATTCGCCAGAAATATACAAGAGCTACAAGTGGCTGCTTTACAACT 545
Qy 659 GCACAAAGCAGAGTGTACAGCTCATGGAACATGACAGTTATATAACGCTTTTGAATCT 718
Db 546 GCCAGAAAGGGTATACAGCTTGATGAGACAACTTATCTCTCGTTCTTGGAGTCA 605
Qy 719 GAGACCTACTTACATTTG 736
Db 606 GAATTTACAGGACTTG 623

RESULT 15

US-09-971-429B-32

;; Sequence 32, Application US/09971429B

;; Publication No. US20030175704A1

;; GENERAL INFORMATION:

;; APPLICANT: Lasek, Amy K. W.

;; APPLICANT: Shyjan, Andrew W.

;; APPLICANT: Turner, Christopher M.

;; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER

;; FILE REFERENCE: PA-0040 US

;; CURRENT APPLICATION NUMBER: US/09/971,429B

;; CURRENT FILING DATE: 2001-10-04

;; PRIOR APPLICATION NUMBER: 60/239,024

;; PRIOR FILING DATE: 2000-04-10

;; NUMBER OF SEQ ID NOS: 56

;; SOFTWARE: PERL Program

;; SEQ ID NO 32

;; LENGTH: 1381

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: misc feature

;; OTHER INFORMATION: Incyte ID No. US20030175704A1 989992.12

US-09-971-429B-32

Query Match 13.1%; Score 152.4; DB 10; Length 1381;

Best Local Similarity 62.7%; Pred. No. 8.9e-23;

Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

Qy 359 TCTCTGAAGAGCAGTGAATGGCTGCAATCATTTGACAAATTTGCTCTCTCATAGAGAT 418

Db 262 TCTCTGAAGAGCAGCAGCTGTGTGTCAGAAATTTGACGAGCTGTAGCCAGCAATAT 321

Qy 419 GGAGTGGATGCTTTTACAGATTTCTTTAAACTGAATTCAGTGGAGGAGCAATTTGAATTT 478

Db 322 GGTCTTGTGTCATTCAGGGCTTTTAAAGTCGGAATTTCTGTGAAGAAATATTTGAATTC 381

Qy 479 TGGCTGGCTGTGAAGCTTCAGAAATGCAAGAACTCAGCAATCATCTCAATCAAAAGCA 538

Db 382 TGGCTGGCTGTGAAGCTTCAGAAATGCAAGAACTCAGCAATCATCTCAATCAAAAGCA 441

Qy 539 AAGCAATCTATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTTTAACTTGAATTT 598

Db 442 AGGAAATATATATCTGACTTCATAGAAAGGAAGCTCCAAAGAGATATAACATAGATTT 501

Qy 599 CATACTAAGAAAGTAAATGCTTAAGAGCATGCCCGAGCCACTCTCCACAGTTTGTATCG 658

Db 502 CAACCAAAACTCTGATTCGCCAGAAATATACAAGAGCTACAAGTGGCTGCTTTACAACT 561

Qy 659 GCACAAAGCAGAGTGTACAGCTCATGGAACATGACAGTTATATAACGCTTTTGAATCT 718

Db 562 GCCAGAAAGGGTATACAGCTTGATGAGAACTCTATCTCTCGTTCTTGGAGTCA 621

Qy 719 GAGACCTACTTACATTTG 736

Db 622 GAATTTACAGGACTTG 639

Search completed: August 20, 2004, 16:40:48

Job time : 546.613 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2004, 06:15:45 ; Search time 462.364 Seconds
(without alignments)
7750.315 Million cell updates/sec

Title: US-09-894-749-3

Perfect score: 1164

Sequence: 1 ttttttaagaaatactga.....gtactagtgcgcgcgc 1164

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5021620 seqs, 1539289099 residues

Total number of hits satisfying chosen parameters: 10043240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
- 8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
- 9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602.6	51.8	1884	8	US-10-115-635-133
2	571.6	49.1	2243	5	US-09-397-206A-5474
3	185.8	16.0	265	5	US-09-397-206A-4445
4	185.6	15.9	289	5	US-09-397-206A-4472
5	183.6	15.8	553	5	US-09-397-206A-1697
6	156.2	13.4	681	7	US-10-488-619-1828
7	155.6	13.4	641	5	US-09-397-206A-3323
8	155	13.3	538	5	US-09-397-206A-3325
9	152.4	13.1	1345	6	US-10-501-035-7
10	152.4	13.1	1345	9	US-09-584-405-119
11	142	12.2	1691	7	US-10-804-491-24
12	142	12.2	1923	7	US-10-100-683-944
13	139	11.9	753	1	PCT-US04-23166-257
14	139	11.9	753	1	PCT-US04-14618-74
15	136.4	11.7	2781	1	PCT-US04-23166-352
16	135.8	11.6	3722	6	US-10-501-933-3396
17	134.8	11.6	440	5	US-09-397-206A-4433
18	134.8	11.6	1489	1	PCT-US04-23166-14
19	134.8	11.6	2919	1	PCT-US04-23166-494
20	132.6	11.4	3327	7	US-10-487-092-60
21	129.8	11.2	1398	1	PCT-US03-27382-25
22	129.8	11.2	1398	1	PCT-US03-04688A-124
23	122.6	10.5	2383	1	PCT-US03-04688A-595
24	122.2	10.5	558	6	US-10-501-933-2472

25	120.6	10.4	955	7	US-10-220-964-3856	Sequence 3856, Ap
26	112.4	9.7	546	5	US-09-969-034-1963	Sequence 1963, Ap
27	108.4	9.3	623	5	US-09-969-034-3013	Sequence 3013, Ap
28	108.2	9.3	1978	6	US-10-896-164-1408	Sequence 1408, Ap
29	108.2	9.3	1978	8	US-10-868-184A-1408	Sequence 1408, Ap
30	108.2	9.3	1978	8	US-10-868-184-1408	Sequence 1408, Ap
31	104.8	9.0	480	9	US-60-568-635-93	Sequence 93, Appl
32	99.6	8.6	1813	8	US-10-115-635-226	Sequence 226, Appl
33	99	8.5	663	1	PCT-US03-03403-47	Sequence 47, Appl
34	94.6	8.1	790	1	PCT-US03-04688A-126	Sequence 126, Appl
35	94.6	8.1	457	7	US-10-488-619-2358	Sequence 2358, Ap
36	94.4	8.1	452	6	US-10-425-115-71747	Sequence 71747, A
37	93.4	8.0	1768	1	PCT-US03-41761-53991	Sequence 53991, A
38	93.4	8.0	1768	1	PCT-US03-41761-53991	Sequence 53991, A
39	93.4	8.0	1768	1	PCT-US03-41766A-53991	Sequence 53991, A
40	89	7.6	591	7	US-10-834-268-4244	Sequence 4244, Ap
41	89	7.6	613	9	US-60-592-408-669	Sequence 669, Appl
42	83.8	7.2	342	5	US-09-796-692B-9309	Sequence 9309, Ap
43	83.8	7.2	342	7	US-10-764-324-9309	Sequence 9309, Ap
44	82.6	7.1	342	5	US-09-796-692B-306	Sequence 306, Appl
45	82.6	7.1	342	5	US-09-796-692B-458	Sequence 458, Appl

ALIGNMENTS

RESULT 1

US-10-115-635-133

; Sequence 133, Application US/10115635

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyun

; APPLICANT: Zhang, Jie

; APPLICANT: Zhao, Qing A.

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wehrman, Tom

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: Novel Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 797CON

; CURRENT APPLICATION NUMBER: US/10/115,635

; CURRENT FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: 09/714,936

; PRIOR FILING DATE: 2000-11-17

; NUMBER OF SEQ ID NOS: 362

; SOFTWARE: pt_FL_genes Version 2.0

; SEQ ID NO 133

; LENGTH: 1884

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (157)..(864)

US-10-115-635-133

Query Match 51.8%; Score 602.6; DB 8; Length 1884;

Best Local Similarity 75.3%; Pred. No. 9.6e-126;

Matches 817; Conservative 0; Mismatches 234; Indels 34; Gaps 4;

QY	1	TTTTTCTAGAAAATCTGAGGAAGATTGGGATAGCGCTTTATTTC-AGGATGTTTTC	59
Db	25	TTCTTTTGTAAACATTACTGTAAGATTGTGATACTTTTATTCTACTATGTAATG	84
QY	60	TATGAATAGCATTCATCTGTGGAGAGAGAGCACTAAGAAATCTGACATCTGTGGT	119
Db	85	TATGAATAGTATTATAAATGAACCTAGGAAGGATGTAATAAATAGACATCTCTCAT	144
QY	120	CATGGGACAGATATGGATATGTCACCTGGTTTCTTCTCAATTAATATGCTGGAAT	179

145 T--TTAGAGAGAGATGAAACCAACATTTCTTTCTTCTCAATAAATATGTGAT 202
180 CAAAAGAGAAACTTTTTCACAACTAATGCGATGGGTGAGGAAAGAGAAACAAGCATCG 239
203 CAAAAGAGAAACTTTTTCACAACTAATGCGATGGGTGAGGAAAGAGAAACAAGCATCG 262
240 AGGCCAATCAGACGCGAAGAGAAAGAAATAGACTAAGTCTCTCTCAGAGGCGTG 299
263 AGGCCAATCAGACGCGAAGAGAAAGAAATAGACTAAGTCTCTCTCAGAGGCGTG 322
300 ACTTCCATCGGAGAGACTCAAGCAGTAGATCGCCCTTTGGCCCAAGAAACAAGAGTCT 359
323 AGTTTCATGAGACACCCGCTCCAGTAGATCGGCGCTTTGGCCCAAGAAACAAGAGTCT 382
360 CTCCTGAGAGAGCAGTGAATGGCGTGAATCATTTGACAAATTTGCTCTCATAGAGATG 419
383 CCCCTGAGAGAGCAGTGAATGGCGTGAATCATTTGACAAATTTGCTCTCATAGAGATG 442
420 GAGTGGATGCTTTTACCAAGATTTCTTAAACTGAACTCAGTGAAGAGAACTTGAATTTT 479
443 GACTAGAGGCTTTTACCAAGATTTCTTAAACTGAACTCAGTGAAGAGAACTTGAATTTT 502
480 GGGTCCCTGTGAAGACTTCAAGAAATGCAAGGAACTCTCAACAAATCATCTTAAAGCAA 539
503 GGATAGCCTGTGAAGATTTCAAGAAAGCAAGGAGCCTCAACAAATTCACCTTAAAGCAA 562
540 AGGCAATCTATGAGAAATTCATTCAGATGATGCCCCCAAGAGGTTAAACATTCATTTTC 599
563 AGCAATATATGAGAAATTTATACAGACTGATGCCCCCAAGAGGTTAAACATTCATTTTC 622
600 ATACTAAAGAAATGCTTAAAGAGCATGCGCCAGCCCACTCTCCACAGTTTTCATACGG 659
623 ACACAAAGAAAGTCAATTAACAACAGCATCACTCAACCTACCTCCACAGTTTTCATGCTG 682
660 CACAAAGCAGAGTGTACAGCTCATGGAACATGAGTAAACGCTTTTGAATCTG 719
683 CACAAAGCAGAGTGTACAGCTCATGGAACATGAGTAAACGCTTTTGAATCTG 742
720 AGACCTACTTACATTTGATAGAGAGAGACCTCAGAGACCAACCAACCTTAGGAGACGAT 779
743 ACATCTATTTAGACTTGTATGAGAGAGACCTCAGAGACCAACCAACCTTAGGAGACGAT 802
780 CACGATCATTTACTTACATGATTTCCAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 839
803 CACGCTCATTTACTGCAATGAATTCACAGATGATCAATCAGATGTTGCCATTTGGTTAT 862
840 GAGTAAAGTCAATTTGCTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 899
863 AAAGAAATTTGATTTGCTCTATTTTATGACAACTTATACATC----- 906
900 ACTAATGTACTTCTTAAATATAGTGTGTATGATGATGATGATGATGATGATGATGATGATGAT 954
907 -----TGCTTCAACATATGCGATGTTTATGTTAAGATTTGGTCCCATCTTTAAA 957
955 -TAAATACACATGCAATATATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1013
958 CTGAATATGATGCAATGTAATTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1017
1014 ATTCATCATCTATCTCCGAATATTTTATGAATCTATCTGATATCTTATCTTAATAA 1073
1018 ATACATACAGTATCTGCCAGTATATCTGTAAACCTTCTATTTGATGATCTCATTCATTA 1077
1074 AATTC 1078
1078 TAATC 1082

RESULT 2

US-09-397-206A-5474

; Sequence 5474. Application US/09397206A

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: MLN98-41PM
; CURRENT APPLICATION NUMBER: US/09/397,206A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,133
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/107,254
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/126,842
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 6473
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5474
; LENGTH: 2243
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2243)
; OTHER INFORMATION: n = A, T, C or G
US-09-397-206A-5474

Query Match 49.1%; Score 571.6; DB 5; Length 2243;
Best Local Similarity 77.3%; Pred. No. 9.3e-119;
Matches 733; Conservative 0; Mismatches 184; Indels 31; Gaps 2;

QY 137 GATATGCTCACTGGTTTCTTCTCTCAATTAATATGTGTGAATCAAAAGAGAGAAACTTTT 196
DB 152 GAAACAACTTCTTTCTTCTTCTCAATTAATATGTGTGAATCAAAAGAGAGAAACTTTT 211
QY 197 TTCAAACTAATCATGGGTTCAGGAAAGAGAAACAAGCATCGAGGCCAAATTCAGACG 256
DB 212 TTCAAGTTAATCATGGTTTCAGGAAAGAGAAACAAGCAAGAGAGAGAGAGAGAGT 271
QY 257 AAAGAAAG 316
DB 272 AAAGAAAG 331
QY 317 CAAGCCAGTAGATCTGCCCTTTGGCCAAAGAGAAACAAGAGTCTCTCTCTCAAGAGAGAG 376
DB 332 CGCTCCAGTAGATCTGGGCACCTTGGCCAAAGAGAAACAAGAGTCTCTCTCTCAAGAGAGAG 391
QY 377 AAATGGGCTGAATCATTTTGAACAAATTTCTCTCTCATAGAGATGGAGTGGATGCTTTTACC 436
DB 392 AAATGGGCTGAATCATTTTGAACAAATTTCTCTCTCATAGAGATGGAGTGGATGCTTTTACC 451
QY 437 AGATTTCTTAAACTCAATTCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 496
DB 452 AGATTTCTTAAACTCAATTCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
QY 497 TTCAAGAAATGCAAG 556
DB 512 TTCAAGAAAG 571
QY 557 TTCAATTCAG 616
DB 572 TTATACAGACTGTATGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
QY 617 GCTAAGAGAGATCGCCAGCCCACTCTCCACAGTTTGTATAGGCAACAAAGAGAGAGTGTAC 676
DB 632 ACAACAGCATCACTCAACCTTACCCTCCACAGTTTGTATAGTGTGTCACAAAGAGAGAGTGTAT 691
QY 677 CAGCTCATGGAACATGACAGTTTATAAACGCTTTTGAATCTGTAGAGAGAGAGAGAGAGAG 736
DB 692 CAGCTCATGGAACATGACAGTTTATACAGTTTCTGAAATCTGTAGAGAGAGAGAGAGAGAG 751
QY 737 ATAGAAG 796
DB 752 ATGAAG 811
QY 797 AATGATTTCCAAG 856

; APPLICANT: Holtzman, Douglas A.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
 ; FILE REFERENCE: HUMAN FETAL SPLEEN LIBRARY
 ; CURRENT APPLICATION NUMBER: US/09/397,206A
 ; CURRENT FILING DATE: 1999-09-17
 ; PRIOR APPLICATION NUMBER: 60/101,133
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/107,254
 ; PRIOR FILING DATE: 1998-11-05
 ; PRIOR APPLICATION NUMBER: 60/126,842
 ; PRIOR FILING DATE: 1999-03-30
 ; NUMBER OF SEQ ID NOS: 6473
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 3325
 ; LENGTH: 538
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(538)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-397-206A-3325

Query Match 13.3%; Score 155; DB 5; Length 538;
 Best Local Similarity 83.2%; Pred. No. 3.2e-25;
 Matches 188; Conservative 0; Mismatches 36; Indels 2; Gaps 1;
 ;
 QY 644 CACAGTTTGTATCGGCACAAAGCAGAGTGATGACGCTCATGGAACATGACATTATAA 703
 DB 4 CCCAGTTTGTATCGGCACAAAGCAGAGTGATGACGCTCATGGAACATGACATTATA 63
 ;
 QY 704 --CGCTTTTGAATCTGAGACCTACTTACATTTGATAGAGGAGACCTCAGAGACAA 761
 DB 64 ACCGTTTCTGAATCTGACATCTATTATGACTTGTAGGAGGAGACCTCAGAGACAA 123
 ;
 QY 762 CAAACCTTAGGAGACGATCAGCATCACTTACATTAATGATTTCCAAAGATGTAAGTCAG 821
 DB 124 CAAATCTTAGGAGACGATCAGCATCACTTACATTAATGATTTCCAAAGATGTAAGTCAG 183
 ;
 QY 822 ATGTGTCATTTGGTTATGATGATTAAGTCATTTGCTCTCTTTGAT 867
 DB 184 ATGTGTCATTTGGTTATGATGATTAAGTCATTTGCTCTCTTTGAT 229

RESULT 9
 US-10-501-035-7
 ; Sequence 7, Application US/10501035
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
 ; FILE REFERENCE: D0185.PCT
 ; CURRENT APPLICATION NUMBER: US/10/501,035
 ; CURRENT FILING DATE: 2004-07-09
 ; PRIOR APPLICATION NUMBER: US 60/350,061
 ; PRIOR FILING DATE: 2002-01-18
 ; NUMBER OF SEQ ID NOS: 795
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 7
 ; LENGTH: 1345
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-501-035-7

Query Match 13.1%; Score 152.4; DB 6; Length 1345;
 Best Local Similarity 62.7%; Pred. No. 1.5e-24;
 Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
 ;
 QY 359 TCTCCTGAGAGCAGTGAATGGGCTGAATCATTTGACAAATGCTCTCTCATAGAGAT 418
 DB 249 TCTCCTGAGAGCAGCTGTGGTCAGAGCATTGACGCTCTGACGAGCAAAATAT 308

QY 419 GGAGTGGATGCTTTTACAGAGATTTCTTAAACTGAATTCAGTGAGAGACATTCGAATTT 478
 DB 309 GGTCTTGTGTCATTCAGGCTTTTTTAAAGTCGGAAATTTCTGTGAAGAAATATTAATTC 368
 ;
 QY 479 TGGGTGCGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTCTAAAGCA 538
 DB 369 TGGGTGCGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTCTAAAGCA 428
 ;
 QY 539 AAGGCAATCTATGAGAAATTCATTGAGATGATGCCCCCAAGAGAGTTTAACATTTGATTT 598
 DB 429 AGGAAATATATATCTGACTTCTAGAAAAGGAGCTCCAAAAGAGATAAACATAGATTTT 488
 ;
 QY 599 CATACTAAAGAGAGTAATTCCTAAGAGCATCGCCAGCCACTCTCCACAGTTTGTATAG 658
 DB 489 CAAACCAAACTCTGATTTGCCAGATATACAAAGAGTACAAAGTGGCTGCTTACAAC 548
 ;
 QY 659 GCACAAAGCAGAGTGATACAGCTCATGGAACATGACAGTTATAAAGCGCTTTTGAATCT 718
 DB 549 GCCCAGAAAAGGATATACAGCTTGTATGAGAGAACTCTTATCCTCGTTTCTTGGAGTCA 608
 ;
 QY 719 GAGACCTACTTACATTTG 736
 DB 609 GAATCTACAGGACTTTG 626

RESULT 10
 US-60-584-405-119
 ; Sequence 119, Application US/60584405
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
 ; FILE REFERENCE: D0185.PCT
 ; CURRENT APPLICATION NUMBER: US/60/584,405
 ; CURRENT FILING DATE: 2004-06-30
 ; NUMBER OF SEQ ID NOS: 527
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 119
 ; LENGTH: 1345
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-60-584-405-119

Query Match 13.1%; Score 152.4; DB 9; Length 1345;
 Best Local Similarity 62.7%; Pred. No. 1.5e-24;
 Matches 237; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
 ;
 QY 359 TCTCCTGAGAGCAGTGAATGGGCTGAATTCATTTGACAAATGCTCTCTCATAGAGAT 418
 DB 249 TCTCCTGAGAGCAGCTGTGGTCAGAGCAATTTGACGAGCTGTAGCCAGCAATAT 308
 ;
 QY 419 GGAGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGAGACATTCGAATTT 478
 DB 309 GGTCTTGTGTCATTCAGGCTTTTTTAAAGTCGGAAATTTCTGTGAAGAAATATTAATTC 368
 ;
 QY 479 TGGGTGCGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTCTAAAGCA 538
 DB 369 TGGGTGCGCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTCTAAAGCA 428
 ;
 QY 539 AAGGCAATCTATGAGAAATTCATTGAGATGATGCCCCCAAGAGAGTTTAACATTTGATTT 598
 DB 429 AGGAAATATATATCTGACTTCTAGAAAAGGAGCTCCAAAAGAGATAAACATAGATTTT 488
 ;
 QY 599 CATACTAAAGAGAGTAATTCCTAAGAGCATCGCCAGCCACTCTCCACAGTTTGTATAG 658
 DB 489 CAAACCAAACTCTGATTTGCCAGATATACAAAGAGTACAAAGTGGCTGCTTACAAC 548
 ;
 QY 659 GCACAAAGCAGAGTGATACAGCTCATGGAACATGACAGTTATAAAGCGCTTTTGAATCT 718
 DB 549 GCCCAGAAAAGGATATACAGCTTGTATGAGAGAACTCTTATCCTCGTTTCTTGGAGTCA 608

QY 719 GAGACCTACTTACATTG 736
|||
Db 609 GAATTCACAGGACTTG 626

RESULT 11

US-10-804-491-24
; Sequence 24, Application US/10804491
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/10/804,491
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/709,103
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 1691
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(587)
; OTHER INFORMATION:
US-10-804-491-24

Query Match 12.2%; Score 142; DB 7; Length 1691;
Best Local Similarity 59.8%; Pred. No. 3.5e-22;
Matches 238; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 341 GCCAAGAAACAGAGTCTCTCTGAGAGAGGAGTGAATGGCTGGAATCATTTGACAAA 400
|||
Db 186 GCCAAGACCCAGAAAACCTCGTGGACGAGGCCCTGCGAGTGGCTGATTCCTCGACAAA 245
|||
QY 401 TTGCTCTCTCATAGAGTGGAGTGCCTTTTACAGATTTCTTAAACTGATTCAGT 460
|||
Db 246 CTCCTGCGAGAACATAGGACTTCCAGATTTCAAAGTTCTTGAAGTCTGAATTCAGT 305
|||
QY 461 GAGGAGAACATGAAATTTGGTGGCTGCTGAGAGCTTCAAGAAATCAAGAAACCTCAA 520
|||
Db 306 GAGGAAACCTTGAGTTCTGAGTTCCTGTGAGGATTACAGAGATCAAGTCCCTGCC 365
|||
QY 521 CAATCATCTTAAAGCAAGGCAATCTATGAGAAATTCATGAGATGATGCCCCCAA 580
|||
Db 366 AAGTGGCTGAGAGGCAAGCAAAATTTATGAGAAATTCATCAACGGAGGCTCCTAAA 425
|||
QY 581 GAGGTTAAACATGATTTTTCATCTAAAGAGTAATTTGTAAGAGCATCGCCAGCCCACT 640
|||
Db 426 GAGGTGAATTTGACCACTTCTCAAGACATCAATGAGAACCTGGTGAACCTTCC 485
|||
QY 641 CTCACAGTTTGTATACGGCAAGAGAGAGTGTACAGCTCATGGAACATGACAGTTAT 700
|||
Db 486 CTGAGCAGCTTTGACATGCGCCAGAAAAGATCCATGCCCTGTATGGAAGAGGATTTCTCTG 545
|||
QY 701 AAACGCTTTTGAATCTGAGACCTTACTTACATTTGAT 738
|||
Db 546 CTCGCTTTGTGGCTCTGAGTTTATCAGGAGTTAT 583
|||

RESULT 12

US-10-100-683-944
; Sequence 944, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162

; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 944
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1910)..(1910)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1912)..(1912)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-100-683-944

Query Match 12.2%; Score 142; DB 7; Length 1923;
Best Local Similarity 59.8%; Pred. No. 3.6e-22;
Matches 238; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 341 GCCAAGAAACAGAGTCTCTCTGAGAGAGGAGTGAATGGCTGGAATCATTTGACAAA 400
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Db 406 GCCAAGACCCAGAAAACCTCGTGGACGAGGCCCTGCGAGTGGCTGATTCCTCGACAAA 465
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QY 401 TTGCTCTCTCATAGAGTGGAGTGCCTTTTACAGATTTCTTAAACTGAAATTCAGT 460
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Db 466 CTCCTGCGAGAACATGAGTTCCTGAGTTCCTGAGTTCCTGAGTTCCTGAGTTCAGT 525
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QY 461 GAGGAGAACATGAAATTTGGTGGCTGCTGAGAGCTTCAAGAAATGCAAGAACTCAA 520
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Db 526 GAGGAAACCTTGAGTTCTGAGTTCCTGAGTTCCTGAGTTCCTGAGTTCCTGAGTTCAGT 585
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QY 521 CAATCATCTTAAAGCAAGCAATCTATGAGAAATTCATTCAGATGATGCCCCCAA 580
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QY 581 GAGGTTAAACATGATTTTTCATCTAAAGAGTAATTTGTAAGAGCATCGCCAGCCCACT 640
|||
Db 646 GAGGTGAATTTGACCACTTCTAAGGACATCAATGAGAACTGGTGAACCTTCC 705
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QY 641 CTCACAGTTTGTATACGGCAAGAGAGTGTACAGCTCATGGAACATGACAGTTAT 700
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Db 706 CTGAGCAGCTTTGACATGCGCCAGAAAAGATCCATGCCCTGTATGGAAGAGGATTTCTCTG 765
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QY 701 AAACGCTTTTGAATCTGAGACCTTACTTACATTTGAT 738
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Db 766 CTCGCTTTGTGGCTCTGAGTTTATCAGGAGTTAT 803
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RESULT 13
PCT-US04-23166-257
; Sequence 257, Application PC/TUS0423166
; GENERAL INFORMATION:
; APPLICANT: Purdue Pharma L.P.
; APPLICANT: Jiefei Tong
; APPLICANT: Gang Jin
; APPLICANT: Rui-Ku Ji
; APPLICANT: Yixun Xu
; APPLICANT: Lillian W. Chiang
; APPLICANT: Daniel J. Lavery
; TITLE OF INVENTION: GENES ASSOCIATED WITH RESPONSES TO NEUROPATHIC PAIN
; FILE REFERENCE: 02755/200M584-W00
; CURRENT APPLICATION NUMBER: PCT/US04/23166
; CURRENT FILING DATE: 2004-07-26
; PRIOR APPLICATION NUMBER: 60/485,101
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 868
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 257
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-23166-257

Query Match	11.9%;	Score 139;	DB 1;	Length 753;
Best Local Similarity	56.6%;	Pred. No. 1.4e-21;		
Matches	278;	Conservative	0;	Mismatches 210; Indels 3; Gaps 1
Qy	251	AGAGCGAAGAAAAGGAATAGACTAGTCTTCTCCTCAGAGGCGTCACTTCATGGA	310	
Db	140	AGTGCAAAAGATATGAACATCGGTAGTTCTCTGCTGCAAAAATCTGATTCCTGTGAA	199	
Qy	311	GAGA---CTCAAGCCAGTAGATCTGCCCTCTTGCCAAAGAAAACAAGAGTCTCTCTGAA	367	
Db	200	CACAATTCITCCCAACAACAAGAGGACAAAGTGGTTATTTGCCAGAGAGTGAGSCCAAGAG	259	
Qy	368	GAAGCAGTGAATGGGCTGAATCATTTGACAAAATGCTCTCTCATAGAGATGAGATGAT	427	
Db	260	GAAGTCAAGAAAATGGGCTGAATCACTGGAAAACCTGATTATGTCATGAATGTGGGCTGGCA	319	
Qy	428	GCCTTTTACCAGATTTCTTAAACACTGAATTCAGTCAGGAGAGAACATTTGAATTTTGGGTCGC	487	
Db	320	GCCTTCAAAGCTTTCTTGAGTCTGAATATATAGTAGGAGAGAAATTTGACTTCTGGATCAGC	379	
Qy	488	TGTGAGAGATTCACAAGAAATGCAAGGAACCTCAACAAATCATCTCTAAAGCAAGGCAATC	547	
Db	380	TGTGAGAGTACAAGAAATCAAATCAACATCTAACTAACTCCCAAGGCCAAAAGATC	439	
Qy	548	TATGAGAAATTCATTACAGATGATGCCCCCAAGAGGTTAACTGATTTTTCATCTATAA	607	
Db	440	TATAATGAATTCATCTCAGTCAGGCAACCAAGAGGTGAACCTGGATTTCTTGACACAGG	499	
Qy	608	GAAGTAATTGCTTAAGAGATCGCCACAGCCCACTCTCCACAGTTTTTGATACGGCAACAAGC	667	
Db	500	GAAGACAAGCGGGAACATGCTAGAGCCTACATAACCTTGCTTTGATGAGGCCCAAGAG	559	
Qy	668	AGAGTGTACAGCTCATGGAACATACACAGTTTATAAAGCTTTTGAATCTCGAGACTAC	727	
Db	560	AAGATTTTCAAACCTGATGGAGAGGATTCCTACCGCGCTTCCTCAAGTCTCGATTCGAT	619	
Qy	728	TTACATTTGAT	738	
Db	620	CTTGATTTGGT	630	

RESULT 14
PCT-US04-14618-74
; Sequence 74, Application PC/TUS0414618
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Olsen, Nancy J
; APPLICANT: Aune, Thomas M
; APPLICANT: Aune, Thomas M

```

; TITLE OF INVENTION: A Gene Equation to Diagnose Rheumatoid Arthritis
; FILE REFERENCE: 1242/64 PCT
; CURRENT APPLICATION NUMBER: PCT/US04/14618
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/468,901
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 2753
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-14618-74

Query Match 11.9%; Score 139; DB 1; Length 2753;
Best Local Similarity 56.6%; Pred. No. 1.9e-21;
Matches 278; Conservative 0; Mismatches 210; Indels 3; Gaps 1;

QY 251 AGAGCGAAGAAAAAGGAATAGACTAAGTCTTCTCTACAGAGCGCTGACTTCCATGGA 310
DB 140 AGTGCAAAAGATGAACATCGCTAGGTTTCTGCTGCAMAAATCTGATTCCTGTGAA 199
QY 311 GAGA---CTCAAGCCAGTAGATGCGCCCTCTTGSCCAAAGAAACAAGAGTCTCTCTGAA 367
DB 200 CACAATTCCTCCACACACAAGAGGACAAAGTGGTTATTTGCCAGAGAGTGAGCCAAAG 259
QY 368 GAAGCAGTGAATGGGCTGAATCATTTTGACAAATTGCTCTCTCATAGAGATGGAGTGGAT 427
DB 260 GAAGTCAGAAATGGGCTGAATCACTGGAAAACTGATTAAGTCATGATGTGGCTGGCA 319
QY 428 GCTTTTACCAGATTTCTTTAAACATGAATCAGTGAGGAGAACATGTAATTTTGGGTGCC 487
DB 320 GCTTTCAAAGCTTCTTGAAGTCTGAATATAGTGAGGAGAAATATGACTTCTTGGATCAGC 379
QY 488 TGTGAAGACTTCAAGAAATCAAGGACCTCAACAAATCATCTTAAAGCAAAGCAATC 547
DB 380 TGTGAAGAGTACAGAAAAATCAATCAACATCTAAATCTAGTCCCAAGGCCAAAAGATC 439
QY 548 TATGAGAAATTCATTCAGAAATGATGCCCCCAAGAGGTTAAATGATTTTATATACTAAA 607
DB 440 TATAATGAATTCATCTCAGTCCAGGCAACCAAGAGGTGAACCTGGATTCTTTGCACCA 499
QY 608 GAAGTAATTCGTAAGAGCATGCGCCAGCCACTCTCCACAGTCTTTGATACGGCACAAAGC 667
DB 500 GAAGAGACAAGCCGGAACATGCTAGAGCCCTACAAATAACCTGCTTTGATGAGGCCCAAG 559
QY 668 AGAGTGACAGCTCATGGAACATGACAGATTAAAGCGTTTTTGAATCTGAGACCTAC 727
DB 560 AAGATTTCAACCTGATGGAGAGGATTCCTACCGCGCTTCTCAAGTCTCGATTCTAT 619
QY 728 TTACATTTGAT 738
DB 620 CTTGATTTGGT 630

RESULT 15
PCT-US04-23166-352
; Sequence 352, Application PC/TUS0423166
; GENERAL INFORMATION:
; APPLICANT: Purdue Pharma L.P.
; APPLICANT: Jiefei Tong
; APPLICANT: Gang Jin
; APPLICANT: Rui-Ru Ji
; APPLICANT: Yixun Xu
; APPLICANT: Lillian W. Chiang
; APPLICANT: Daniel J. Lavery
; TITLE OF INVENTION: GENES ASSOCIATED WITH RESPONSES TO NEUROPATHIC PAIN
; FILE REFERENCE: 02755/200M584-WO
; CURRENT APPLICATION NUMBER: PCT/US04/23166
; CURRENT FILING DATE: 2004-07-26
; PRIOR APPLICATION NUMBER: 60/485,101
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 868

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US04-23166-352

Query Match 11.7%; Score 136.4; DB 1; Length 2781;
Best Local Similarity 56.3%; Pred. No. 7.2e-21;
Matches 276; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

Qy	251	AGAGCGAAGAAAAGGATAGACTAAGTCTCTCTACAGAGCGCTGACTTCATGGA	310
Db	140	AGTGAAGGACATGAACATCGGCTGGGGTCTCTGCTGCAAGATCAGATTCTCGCGAA	199
Qy	311	GAGA---CTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAACAAGAGTCTCTCTGAA	367
Db	200	CACAGTCTTTCACACAGCAAGAGGACAAGTAGTAACTTGCAGAGGGTAAAGCAAGAA	259
Qy	368	GAAGCAGTGAATGGGCTGAATCATTTGACAAATTCCTCTCTCATAGATGAGTGGAT	427
Db	260	GAAGTCAAGAAATGGGCTGAATCGTTGGAACCTGATTCCACCATGAATGTGACTGCA	319
Qy	428	GCTTTTACAGATTTCTTAAACTGAATTCAGTGAAGGAGAACATTTGCGGTGCGC	487
Db	320	GCTTTCAAGCTTCTCTGAGTGGATATACGCGAGGAGAACATTGACTTCTGGATCAGC	379
Qy	488	TGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAATCATCTAAAGCAAGGCAATC	547
Db	380	TGTGAGGAGTACAAAGAAATCAAGTCACCTTCTAAACTAAGTCCCAAGCCCAAGAGATC	439
Qy	548	TATGAGAAATTCATTCAAGATGATGCCCAAGAGGTTAATTCATTTCATCTAAA	607
Db	440	TACAAGAGTTTCACTCTCAGTGAAGCAACAAGAGGTGAACCTGACTCTTTGACCCAGA	499
Qy	608	GAAGTAATTGCTAAGAGCATCGCCAGCCCACTCTCCACAGTTTGTATACGGCACAAAGC	667
Db	500	GAGGAGACAAGCCGGAACATGTTACAGCCCAACAATAACCTGTTTGTATGAAGCCCAAG	559
Qy	668	AGAGTGTACAGCTCATGGAACATGACAGTTTATAACGCTTTTGAATCTGAGACCTAC	727
Db	560	AAGATTTTCAACCTGATGGAAGAGGATTCCTACCGCGCTTCTCAAGTCTCGATTCTAT	619
Qy	728	TTACATTGA	737
Db	620	CITGACCTGA	629

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Job time : 464.364 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2004, 05:11:40 ; Search time 3157.02 Seconds
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Total number of hits satisfying chosen parameters: 55026578

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: em_hct:
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10: gb_est2:
11: gb_hct:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rod:
26: em_gss_pbg:
27: em_gss_vrl:
28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1116.4	95.9	1860	11 AX036407	AX036407 Mus muscu
2	605.4	52.0	700	13 BY750625	BY750625 BY750625
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13	402.8	34.6	810	12 BG564257
14	392.2	33.7	705	9 AV714060
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33	275	23.6	351	13 BY111479
34	270.2	23.2	339	13 BY215437
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37	252.6	21.7	648	28 AZ084304
38	242.8	20.9	610	9 AI981146
39	242.6	20.8	694	13 BU277880
40	240.8	20.7	676	14 CB018381
41	238.4	20.5	632	12 EQ038335
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ALIGNMENTS

RESULT 1
AK036407
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK036407 1860 bp mRNA linear HTC 19-SEP-2003
Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:983000610 Product:regulator of G-protein signaling 18, full insert sequence.

AK036407 GI:26331373
HTC; CAP trapper.
Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3
REFERENCE
AUTHORS
 Shibata.K., Itoh.M., Aizawa.K., Nagaoka.S., Sasaki.N., Carninci.P.,
 Konno.H., Akiyama.J., Nishi.K., Katsunai.T., Teshiro.H., Itoh.M.,
 Sumi.N., Ishii.Y., Nakamura.S., Hazama.M., Nishine.T., Harada.A.,
 Yamamoto.R., Matsumoto.H., Sakaguchi.S., Ikegami.T., Kashiwagi.K.,
 Fujiwake.S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E., Watahiki.M.,
 Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka.T., Matsura.S., Kawai.J.,
 Okazaki.Y., Muramatsu.M., Inoue.Y., Kira.A. and Hayashizaki.Y.
TITLE
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
REFERENCE
AUTHORS
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium
TITLE
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 695-690 (2001)
 5
REFERENCE
AUTHORS
 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team
TITLE
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 1860)
 Fuchida,S., Aizawa.K., Akimura.T., Arakawa.T., Bono.H., Carninci,P.,
 Adachi,J., Furuno.M., Hanagaki.T., Hara.A., Hashizume.W.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka.T., Hirozane.T.,
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 Sogabe.Y., Tagami.M., Tagawa,A., Takahashi.F., Takaku-Akahira,S.,
 Takeda.Y., Tanaka.T., Tomaru,A., Toya.T., Yasunishi,A.,
 Muramatsu,M. and Hayashizaki,Y.
TITLE
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.go.jp/
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 1839. .1844
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 1860
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 polyA_site
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 Query Match 95.9%; Score 1116.4; DB 11; Length 1860;
 Best Local Similarity 99.9%; Pred. No. 4.3e-227;
 Matches 1117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 109 ATGAAATAGCATTCATCTGTGGGAGAGAGAGACTAAGGAAATCTGACATCTGTTGGTC 168
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 DB 229 AAAAGAGAAAACTTTTTCATAACTTAATGTCATGGGTGAGGAAAGAGAAACAAGCATCGA 288
 QY 241 GGCCTAATCAGACGCGAAGAAAGAAAGGATGACATTAAGTCTTCTCTCAGAGGCGCTGA 300
 DB 289 GGCCTAATCAGACGCGAAGAAAGAAAGGATGACATTAAGTCTTCTCTCAGAGGCGCTGA 348
 QY 301 CTTCATCTGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAACAAGAGTCTC 360
 DB 349 CTTCATCTGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAACAAGAGTCTC 408
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 DB 829 ACGATCAATTTACTTACAAATGATTTCCAGATGTAAGTGAAGTGTGCGCATTTGGTTATG 888
 QY 841 AGTAAAGTCAATTTGCTCTCTTTTGATGTGTATGTATATCTATAATATATACTAATA 900

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Db      889 AGTAAAGTCATTTGCTCTTTTCATAGTGATGTGTATATCTCTAAATATATACTAATA 948
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Qy      1021 AFTATCTTCGAAATATTTTATGAATAATCTATCTGATATCTATCTATTAATAAATTTT 1080
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RESULT 2
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LOCUS   BY750625 700 bp mRNA linear EST 17-DEC-2002
DEFINITION BY750625 RIKEN full-length enriched, activated spleen Mus musculus
          CDNA clone F830007B06 5', mRNA sequence.
ACCESSION BY750625
VERSION   BY750625.1 GI:27180611
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 700)
Okazaki, Y., Oate, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Goljebori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Batalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusic, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Perteau, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Seiple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, I. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354693
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Arahata, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, E.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipipillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Matches 623; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
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Qy      121 ACTGGGACAGAATATGGATATGTCACTGGTTCCTCTCTCAATTAATATGTGTAATC 180
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Qy      181 AAAAGAGAAAACCTTTTCAAACTAATGATGGTGTAGGAGAAAGAGAAACAAGATCGA 240
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Qy      241 GGCCAAAATCAGAGCGGAGAAAGAAAGGAATAGACTAAGTCTTCTCTACAGAGGCGCTGA 300
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Qy      301 CTTCCATGGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAAACAAGAGTCTC 360
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Qy      361 TCCTGAAGAGCGAGTGAATGGCTGAATCATTTGACAAATTCCTCTCTCATGAGATGG 420
Db      420 TCCTGAAGAGCGAGTGAATGGCTGAATCATTTGACAAATTCCTCTCTCATGAGATGG 479

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RESULT 3
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LOCUS AL557903 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DJ003YU10 5-PRIME, mRNA sequence.
ACCESSION AL557903
VERSION AL557903.2 GI:31279703
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
CONTACT On Feb 15, 2001 this sequence version replaced gi:12901962.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 261.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seg=CS0DJ003DE050P1&cluster=261.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
Query March 51.1%; Score 594.4; DB 9; Length 1201;
Best Local Similarity 81.0%; Pred. No. 4.1e-116;
Matches 714; Conservative 2; Mismatches 163; Indels 3; Gaps 2;

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LOCUS Mus musculus HCV7202 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY420374
VERSION AY420374.1 GI:39776331
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 655)
Clark, A.G., Glandowski, S., Nielson, P., Thomas, P., Kejarawal, A.,
Todd, M.A., Fandenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

```

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 655)
AUTHORS Clark.A.G., Gnanowski.S., Nielson.R., Thomas.P., Kejarawal.A., Todd.M.A., Tanenbaum.D.M., Civello.D.R., Lu.F., Murphy.B., Perrier.A.S., Wang.G., Zheng.X.H., White.T.J., Sninsky.J.J., Adams.M.D. and Cargill.M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
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Matches 655; Conservative 0; Mismatches 0; Indels 53; Gaps 1;
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Db 608 TACAATGATTTCAAGATGTAAGTCAGATGTTGCCATTTGGTTATGA 655

RESULT 5
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DEFINITION BB660526 RIKEN full-length enriched, 13 days embryo stomach Mus
ACCESSION BB660526
VERSION BB660526.1 GI:16494345
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 666)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,I., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
UNPUBLISHED (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Shuho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
Location/Qualifiers
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/clone.lib="RIKEN full-length enriched, 13 days embryo stomach"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
 GAGAGAGAGCGGCGCAACTCGATGTTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5']
 GAGAGAGATCTGAGTTAATAATTAATCCCGCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 48.2%; Score 560.8; DB 10; Length 666;
 Best Local Similarity 95.8%; Pred. No. 5.8e-109;
 Matches 585; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

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Db	175	ACTGGGACAGAAATATGATATGATGCTGCTTTCTCTCTCAATTAATATGTGAATC	234
QY	181	AAAGAGAGAAAC-TTTTTTCAACTAATGATGGTTCAGGAAAGAGAAACAACATCG	239
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QY	360	CTCCTGAAGAGAGAGTGAATGGCTGAATCTTTTTCATTAATGCTCTCTCATGAGATG	419
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QY	420	GAGTGAATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAGAACATTTGATTTT	479
Db	475	GAGTGAATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAAGAGAACATTTGATTTT	534
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QY	540	AGGCAATCTATGAAATTCATTTCAGAAATGTCGCCCAAGAGGTTAATGATTTTC	599
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QY	600	ATACTAAAGAG 611	
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RESULT 6
 BY722727
 LOCUS
 DEFINITION
 cDNA clone 9830132K19 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY722727 618 bp mRNA linear EST 17-DEC-2002
 BY722727 RIKEN full-length enriched, adult male bone Mus musculus
 cDNA clone 9830132K19 5', mRNA sequence.
 BY722727
 EST
 Mus musculus (house mouse)
 Mus musculus
 Fukuyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 618)
 Okazaki, Y., Furuno, M., Kusukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Kikaido, I., Osato, N., Saito, R., Suzuki, H., Yamashita, I.,
 Kiyosawa, H., Yagi, K., Tomari, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
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 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
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 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Varardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wyszewski-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
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 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
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 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

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 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
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Email: genome-res@sc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES
 Location/Qualifiers
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ORIGIN

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QY	1	TTTTTTGACAAAAATCTGAGGAAAGATTCTGGGATAGCGCTTTATTTCAGGATGTTTTTCCT	60	
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QY	61	ATGAAATAGCATTCATCTCTGGGAGAGAGAAGACTAAGGAAATCTGACATCTGTGGTC	120	
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QY	181	AAAAGAGAAAACCTTTTTTCAAATTAATGTCATGGGTACGGGAAGAGAAACACAGCATCGA	240	
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Db	596	GGCAATCTATGAGAAATTCATTC	618	

RESULT 7
BU698389
LOCUS

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DEFINITION      LL2in13951T7 Hematopoietic Stem Cell Subtracted Library Mus
                 musculus cDNA 5' similar to RGP5, regulator of G-protein
                 signalling, mRNA sequence.
ACCESSION       BU698389
VERSION         BU698389.1  GI:23611104
KEYWORDS        EST.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE       1 (bases 1 to 538)
                Phillips,R.L., Ernst,R.E., Brunk,B.P., Ivanova,N., Mahan,M.A.,
                Deanehan,J.K., Moore,K.A., Overton,G.C. and Lemischka,I.R.
                The genetic program of hematopoietic stem cells
                Science 288 (5471), 1635-1640 (2000)
JOURNAL         20295303
MEDLINE         10834841
PUBMED         10834841
COMMENT         Contact: Lemischka, Ihor R.
                Department of Molecular Biology
                Princeton University
                Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA
                Tel: 609 258 2838
                Fax: 609 258 2759
                Email: ilemischka@molbio.princeton.edu
                These ESTs are derived from a subtracted cDNA library enriched for
                stem products expressed in day 14-14.5 fetal liver hematopoietic
                stem cells defined as Lineageneg/lo, AA4.lpos, ckItpos, Ly6A/E
                (Sca-1)pos
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                    enriched to be Lineageneg/lo, AA4.lpos, ckItpos, Ly6A/E
                    (Sca-1)pos called Scapos and from AA4.lneg fetal liver
                    cells. Subtractive hybridization was performed by
                    hybridization of the target, Scapos, single stranded cDNA
                    library in pSport1 to biotinylated RNA transcribed from
                    the driver, AA4.lneg cDNA library in pSport2 with inserts
                    cloned in the complementary orientation. For detailed
                    protocols and additional information please see our
                    website at http://stemcell.princeton.edu."

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ORIGIN

	Query Match	46.1%;	Score 536.4;	DB 13;	Length 538;
	Best Local Similarity	99.8%;	Pred. No. 9.1e-104;		
	Matches 537;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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QY	335	CTCTTGGCCAA	GAAGAAACAAGAGTCT	CTCCTGAGAGACAGTGA	AGTAATGGGCTGAATCATTT 394
DB	61	CTCTTGGCCAA	GAAGAAACAAGAGTCT	CTCTTGAAGACAGTGA	AGTAATGGGCTGAATCATTT 120
QY	395	GACAAATGCTC	TCTCATAGAGATGGAGTGGAT	GTCTTTTACCGATTTCTT	TAAACCTGAA 454
DB	121	GACAAATGCTC	TCTCATAGAGATGGAGTGGAT	GTCTTTTACCGATTTCTT	TAAACCTGAA 180
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RESULT 8
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LOCUS      708 bp      DNA      linear      GSS 12-DEC-2003
DEFINITION Homo sapiens HCM7202 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION  AY420372
VERSION     AY420372.1  GI:39776329
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 708)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
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            Science 302 (5652), 1960-1963 (2003)
14671302
REFERENCE   2 (bases 1 to 708)
AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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            This sequence as made by sequencing genomic exons and ordering them
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Qy      614  ATTGCTAAGAGCATGCGCCAGCCCACTCTCCACAGTTTTTGTATACGGCACAAGCAGAGT 673
Db      481  ATTACAAACAGCATCACTCAACCTACCTCCACAGTTTGTATGCTGCACAAGCAGAGT 540
Qy      674  TACAGCTCATGGAACATGACAGTTATAACGCTTTTGAATCTGAGACCTTACTTACAT 733
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LOCUS      616 bp      mRNA      linear      EST 26-OCT-2001
DEFINITION BB629298 RIKEN full-length enriched, adult male bone Mus musculus
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ACCESSION  BB629298
VERSION     BB629298.1  GI:16466502
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 616)
            Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
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            Sugabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
            Unpublished (2001)
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center (GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,

```

URL: <http://genome.gsc.riken.go.jp/>
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K. I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.

FEATURES source

1. .616
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 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTT 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGAGTTAAATTAATCCGCCGCC sequence [5' GAGAGAGATCTCGAGTTAAATTAATCCGCCGCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda **FLC1.**"

ORIGIN

Query Match 42.4%; Score 493.8; DB 10; Length 616;
 Best Local Similarity 98.6%; Pred. No. 1e-94;
 Matches 498; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TTTTCTAAGAAAATCTCAGGAAGATTCGGATAGCGCTTTATTCAGGATGTTTCT 60
 DB 46 TTTTCTAAGAAAATCTCAGGAAGATTCGGATAGCGCTTTATTCAGGATGTTTCT 105
 QY 61 ATGAATACATTCATCTCTGGAGAGAGAGCTAAGGAATCTGACATCTGTTGGTC 120
 DB 106 ATGAATACATTCATCTCTGGAGAGAGAGCTAAGGAATCTGACATCTGTTGGTC 165
 QY 121 ACTGGACAGATATGATATGCTACCTGGTTTCTTCTCAATTAATATGTTGAATC 180
 DB 166 ACTGGACAGATATGATATGCTACCTGGTTTCTTCTCAATTAATATGTTGAATC 225
 QY 181 AAAAGAAAACCTTTTCAACTAATGATGGTTCAGGGAAGAGAAACAGCATCGA 240

DB 226 AAAAGAAAACCTTTTCAACTAATGATGGTTCAGGGAAGAGAAACAGCATCGA 285
 QY 241 GGCCTAATCAGAGCAGAAAGAAAAGGAATAGACTAAGTCTTCTCTACAGAGGCTGA 300
 DB 286 GGCCTAATCAGAGCAGAAAGAAAAGGAATAGACTAAGTCTTCTCTACAGAGGCTGA 345
 QY 301 CTTCATGGAGAGACTCAAGCCAGTAGATCGCCCTTTCGCCCAAGAAAACAGAGTCTC 360
 DB 346 CTTCATGGAGAGACTCAAGCCAGTAGATCGCCCTTTCGCCCAAGAAAACAGAGTCTC 405
 QY 361 TCCTGAGAGAGCAGTGAATGGCTGATCATTTGACAAATTCCTCTCATGAGATGG 420
 DB 406 TCCTGAGAGAGCAGTGAATGGCTGATCATTTGACAAATTCCTCTCATGAGATGG 465
 QY 421 AGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGAGAACATTTGAATTTG 480
 DB 466 AGTGGATGCTTTTACCAGATTTCTTAAACTGAATTCAGTGAGAGAACATTTGAATTTG 525
 QY 481 GGTGCTCTGTGAAGACTTCAAGAAA 505
 DB 526 GGTGCTCTGTGAAGACTTCAAGAAA 550

RESULT 10 CD466872

LOCUS CD466872 661 bp mRNA linear EST 04-JUN-2003
 DEFINITION LeukON2_8 B10.g1 A024 Unstimulated peripheral blood leukocytes N2
 Equus caballus cDNA clone LeukON2_8 B10 A024 5', mRNA sequence.
 ACCESSION CD466872
 VERSION CD466872.1 GI:31388140
 KEYWORDS EST.
 SOURCE Equus caballus (horse)
 ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 REFERENCE 1 (bases 1 to 661)
 AUTHORS Moore, J.N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L.H.
 TITLE An EST database from equine (Equus caballus) unstimulated peripheral blood leukocytes
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: LeukON2_8 B10.b2 A024
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
 Seq primer: Sug5 (CTTGTGCTCTAAAGCTGCG).

FEATURES source

1. .661
 /organism="Equus caballus"
 /mol_type="mRNA"
 /strain="thoroughbred"
 /db_xref="taxon:9796"
 /clone="LeukON2_8 B10 A024"
 /sex="male"
 /tissue_type="blood"
 /cell_type="leukocytes"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_lib="Unstimulated peripheral blood leukocytes N2"
 /note="Organ: circulatory system; Vector: pME188-FL3;
 Site_1: XhoI; Site_2: XhoI; The library was prepared from

/clone lib="NIH_MGC 76"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggcgctggcc); Site 2: SfiI (ggcgctggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGCGCTATGCGC-3' and 3' adaptor sequence:
 5'-ATTCTAGCGCGCGCGGACATG-dr(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 34.6%; Score 402.8; DB 12; Length 810;
 Best Local Similarity 75.2%; Pred. No. 2.2e-75;
 Matches 582; Conservative 0; Mismatches 182; Indels 10; Gaps 6;

QY 1 TTTTCTAGAAAATCTGAGGAAGATTCGGGATAGCGCTTATTC-AGGATGTTTCC 59
 DB TTTTCTAGAAAATCTGAGGAAGATTCGGGATAGCGCTTATTC-AGGATGTTTCC 59
 QY 38 TTTTCTAGAAAATCTGAGGAAGATTCGGGATAGCGCTTATTC-AGGATGTTTCC 97
 DB TTTTCTAGAAAATCTGAGGAAGATTCGGGATAGCGCTTATTC-AGGATGTTTCC 97
 QY 60 TATGAATAGCATCTCTGCGGAGAGAGGACTAAGGAATCTGACATCTCTGCT 119
 DB TATGAATAGCATCTCTGCGGAGAGAGGACTAAGGAATCTGACATCTCTGCT 119
 QY 98 TATGAATAGCATCTCTGCGGAGAGAGGACTAAGGAATCTGACATCTCTGCT 157
 DB TATGAATAGCATCTCTGCGGAGAGAGGACTAAGGAATCTGACATCTCTGCT 157
 QY 120 CACTGGGACAGATATGATATGCTACTGGTCTCTCTCTCAATTAATATGTTGAT 179
 DB CACTGGGACAGATATGATATGCTACTGGTCTCTCTCTCAATTAATATGTTGAT 179
 QY 158 T-TTAGAGAGAGATGGAACAACATCTGCTTTCTTCTCAAAATAATATGTTGAT 215
 DB T-TTAGAGAGAGATGGAACAACATCTGCTTTCTTCTCAAAATAATATGTTGAT 215
 QY 180 CAAAAGAGAAACCTTTTCAAACTAATCATGGTGGTCAAGGA-AGAAGAAACAAGCATC 238
 DB CAAAAGAGAAACCTTTTCAAACTAATCATGGTGGTCAAGGA-AGAAGAAACAAGCATC 238
 QY 216 CAAAAGAGAAACCTTTTCAAGTTAATCATGGTTCAGAACACAGAGAAACAAGCAA 275
 DB CAAAAGAGAAACCTTTTCAAGTTAATCATGGTTCAGAACACAGAGAAACAAGCAA 275
 QY 239 GAGGCCAAATCAGCGGAAAGAAAAGGAATAGACTAAGTCTTCTCTCAGAGGCT 298
 DB GAGGCCAAATCAGCGGAAAGAAAAGGAATAGACTAAGTCTTCTCTCAGAGGCT 298
 QY 276 GAAGCCAAATCAGAGCTAAGGAACCAAGACATAGACTAAGTCTTCTGCGAAGACCT 335
 DB GAAGCCAAATCAGAGCTAAGGAACCAAGACATAGACTAAGTCTTCTGCGAAGACCT 335
 QY 299 GACTTCCATGAGAGACTCAAGCCATAGATCTGCCCTTCTGCGCAAGAACAGAGTGC 358
 DB GACTTCCATGAGAGACTCAAGCCATAGATCTGCCCTTCTGCGCAAGAACAGAGTGC 358
 QY 336 GAGTTTCATGAGACACCCGCTCCAGTAGATCTGGGCACTTGGCCAAAGAAACAAGATC 395
 DB GAGTTTCATGAGACACCCGCTCCAGTAGATCTGGGCACTTGGCCAAAGAAACAAGATC 395
 QY 359 TCTCTCAAGAGACAGTGAATGGGCTGAATCATTTGACAAATGCTCTCTCATAGAGAT 418
 DB TCTCTCAAGAGACAGTGAATGGGCTGAATCATTTGACAAATGCTCTCTCATAGAGAT 418
 QY 396 TCCCTGAGAGGCGAGTGAATGGGCTGAATCATTTGACAAATGCTCTTCCATAGAGAT 455
 DB TCCCTGAGAGGCGAGTGAATGGGCTGAATCATTTGACAAATGCTCTTCCATAGAGAT 455
 QY 419 GAGTGGATGCTTTTACAGATTTCTTAAACTGAATTCAGTGAGGAGAACATGAAATTT 478
 DB GAGTGGATGCTTTTACAGATTTCTTAAACTGAATTCAGTGAGGAGAACATGAAATTT 478
 QY 456 GGACTAGAGGCTTTTACAGATTTCTTAAACTGAATTCAGTGAGGAGAACATGAAATTT 515
 DB GGACTAGAGGCTTTTACAGATTTCTTAAACTGAATTCAGTGAGGAGAACATGAAATTT 515
 QY 479 TGGGTCGCTGTGAAGACTTCAAGAAATCAAGGAACCTCAACAATCATCTTAAAGCA 538
 DB TGGGTCGCTGTGAAGACTTCAAGAAATCAAGGAACCTCAACAATCATCTTAAAGCA 538
 QY 516 CGGATAGCTGTGAAGATTTCAAGAAACCAAGGACCTCAACAATTCACCTTAAAGCA 575
 DB CGGATAGCTGTGAAGATTTCAAGAAACCAAGGACCTCAACAATTCACCTTAAAGCA 575
 QY 539 AAGGCAATCTATGAG-AAATTCATTCAGAAATGATGCCCCCAAGAGGTTAACTTGATTT 597
 DB AAGGCAATCTATGAG-AAATTCATTCAGAAATGATGCCCCCAAGAGGTTAACTTGATTT 597
 QY 576 AAAGCAATATATGAGCAAAATTTATACAGACTGATGCCCCCAAGAGGTTAACTTGATTT 635
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 QY 598 T--CATACTAAAGAGTAAATGCTAAGAGCATGCGCCAGCCACCTCCACAGTTTTCAT 655
 DB T--CATACTAAAGAGTAAATGCTAAGAGCATGCGCCAGCCACCTCCACAGTTTTCAT 655
 QY 636 TTCACACCAAAAGAGTCAATTAACAACATCATCTCAAGCTACCTCCACATGTTTTCAT 695
 DB TTCACACCAAAAGAGTCAATTAACAACATCATCTCAAGCTACCTCCACATGTTTTCAT 695
 QY 656 ACGGCAAAA---GCAGAGTGATCCAGCTCATGGAACATGACAGTTATAAAGCTTTTTC 712
 DB ACGGCAAAA---GCAGAGTGATCCAGCTCATGGAACATGACAGTTATAAAGCTTTTTC 712
 QY 696 GCTGCACAAAAGCAGAAAGTATCAGCTCCATGATGGAACAAGACAGTATACAGCTCTCCT 755
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 QY 713 AAATCTGACACTTACTTATTTAGTAGAGAGAGACCTCAGAGACCAAC 765
 DB AAATCTGACACTTACTTATTTAGTAGAGAGAGACCTCAGAGACCAAC 765
 QY 756 AAATCTGACACTTATTTAGTAGAGAGAGACCTTCCGAGACCAAC 809
 DB AAATCTGACACTTATTTAGTAGAGAGAGACCTTCCGAGACCAAC 809

RESULT 14
 AV714060
 LOCUS

DEFINITION AV714060 DCB Homo sapiens cDNA clone DCBBIF02 5', mRNA sequence.
 ACCESSION AV714060
 VERSION AV714060.1 GI:10795577
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 705)
 AUTHORS Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
 Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
 Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
 Lu,G., Cheng,Z. and Han,Z.
 TITLE Homo sapiens cDNA DCB clones
 JOURNAL Unpublished (2000)
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 FEATURES
 Location/Qualifiers
 1..705
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DCBBIF02"
 /cell_type="dendritic cells"
 /dev_stage="mature"
 /lab_host="BM25.8"
 /clone_lib="DCB"
 /notes="Vector: pTriplex2; Site_1: sfiI; Site_2: sfiIB"

ORIGIN
 Query Match 33.7%; Score 392.2; DB 9; Length 705;
 Best Local Similarity 80.1%; Pred. No. 4e-73;
 Matches 486; Conservative 0; Mismatches 118; Indels 3; Gaps 2;

QY 4 TTCTAGAAAAATCTCAGGAAAGATTCGGGATAGCGCTTTATTC-AGGATGTTTCTCTAT 62
 DB TTCTTTGTAAACATTAAGTGTAGAGTTGTGATAAATTTTATTTCTACTATGATATGAT 100
 QY 63 GAATAGCATTCATCTCTGGGAGAGAGGAGTCTAGGAAATCTGACATCTGTTGTCAC 122
 DB TTTTGTGTTTAAATAAGTAACTAGGAGGATGTAATAAATTAGACATCTCTTCAAT 158
 QY 123 TGGGACAGAAATATGGATATGTCATGCTGTTTCTCTCAATTTAAATATGTGAAATCAA 182
 DB TTAGAGAGAGATGGAACAACATGCTTTCTTCTCAATAAATAATATGTGAAATCAA 218
 QY 183 AAGAGAAATCTTTTCAAACTAATGCTGCTGAGGAGAGAGAGAAACAAGCATCGAG 242
 DB AAGAGAAATCTTTTCAAGTTAATCATGTTTCAGGAAAGAGAGAAACAAGCAAGAAG 278
 QY 243 CCAAAATCAGAGCGAAGAAAAAGGAAGTAAGTCTTCTCTACAGAGCCCTGACT 302
 DB CCAAAATCAGAGCTAGGAAAGAAAGTAAGTCTTCTTGTGCGAGAACCTGACT 338
 QY 303 TCCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGCCCAAGAAACAAGAGTCTCTC 362
 DB TCCATGAGAGACTCAAGCCAGTAGATCTGCCCTCTTGCCCAAGAAACAAGAGTCTCCC 398
 QY 363 CTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTTGCTCTCTATAGAGTGGAG 422
 DB CTGAAGAGCAGTGAATGGGCTGAATCATTTGACAAATTTGCTTCCATAGAGTGGAG 458
 QY 423 TGGATGCTTTTACAGATTTCTTAAACTGAATTCAGTCTGAGGAGAACATTTGAATTTGGG 482
 DB TAGAGGCTTTTACAGATTTCTTAAACTGAATTCAGTCTGAGGAGAACATTTGAATTTGGA 518
 QY 483 TCGCCCTGTGAGACTTCAAGAAATGCAAGGAACCTCAACAATCATCTCTTAAAGCAAGG 542

Db 519 TAGCCTGTGAAGATTTCAGAAAGCAAGGACCTCAACAAATTCACCTTAAGCAAAAG 578
 Qy 543 CAATCTATGAGAAATTCATTCAGATGATGCCCCCAAGAGGTTAACATTTTCATA 602
 Db 579 CAATATATGAGAAATTTATACAGACTGATGCCCCCAAGAGGTTAACCTTTTACAA 638
 Qy 603 CTAAAGA 609
 Db 639 CTGCACA 645

RESULT 15
 AV714044
 LOCUS AV714044 DCB Homo sapiens cDNA clone DCEFH06 5', mRNA sequence.
 DEFINITION
 ACCESSION AV714044
 VERSION AV714044.1 GI:10795561
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
 Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
 Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
 Lu,G., Cheng,Z. and Han,Z.
 Homo sapiens cDNA DCB clones
 Unpublished (2000)
 CONTACT: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

LOCATION/Qualifiers
 1..626

FEATURES
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 1..626
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DCBFH06"
 /cell_type="dendritic cells"
 /dev_stage="mature"
 /lab_host="BM25.8"
 /clone_lib="DC3"
 /note="Vector: pTriplEx2; Site_1: sf11A; Site_2: sf11B"

ORIGIN

Query Match 33.3%; Score 387.8; DB 9; Length 626;
 Best Local Similarity 80.0%; Pred. No. 3.5e-72;
 Matches 481; Conservative 0; Mismatches 117; Indels 3; Gaps 2;
 Qy 4 TTGTAGAAATAATCTGAGAAAGATTGGGATAGCGCTTATTTC-AGGATGTTTTCCTAT 62
 Db 28 TTTTGTGTAACATTACTGTAGAGTTGTGATACTTTTATTTCTACTGTATATGTAT 87
 Qy 63 GAAATAGCATTCATCTGTGGGAGAGAGAGGACTAGGAAATCTGACATCTGTGGTCAC 122
 Db 88 GGAATAGTATTAATAAATGAACCTAGGAGAGGATGTAATAAATTAGACATCTCTCAAT-- 145
 Qy 123 TGGGACAGAAATGATATGTCTACCTGGTTTCTCTCTCAATTAATATGTGTAATCAA 182
 Db 146 TTAGAGAGAGATGGAACAACAATTCCTTTTCTTCTCAATTAATATGTGTAATCAA 205
 Qy 183 AAGAGAAAACTTTTTCAAACTAATGATGCGTCAAGGAAAGCAAGAAACAAGCATCGAGG 242
 Db 206 AAGAAAAAACTTTTTCAGTTTAATACATGTTTCAGGAAAGCAAGAAACAAGCAAGAAAG 265
 Qy 243 CCAAAATCAGAGCGAAGAAAGGAATAGACTAGTCTTCTCTCAGAGGCGCTGACT 302

Db 266 CCAAAATCAGAGCTAAGGAAAAAAGAAATAGACTAAAGTCTTCTGTGCGAAAAACCTGAGT 325
 Qy 303 TCATGAGAGAGCTCAAGCCAGTAGATCTGCCCTCTTGGCCAAAGAAAAACAAGAGTCTCTC 362
 Db 326 TTATGAGACACCCGCTCCAGTAGATCTGGGCACCTTGGCCAAAGAAACAAGAGTCTCCC 385
 Qy 363 CTGAAGAAGCAGTGAATGGGCTGAATCTATTGACAAATTTGCTCTCTCATAGAGATGGAG 422
 Db 386 CTGAAGAGGCAGTGAATGGGCTGAATCTATTGACAAACTGCTTTCCCATAGAGATGGAC 445
 Qy 423 TGGATGCTTTTACCAGATTTCTTTAAAACTGAATTCAGTGAAGGAGAACATTGAATTTGGG 482
 Db 446 TAGAGGCTTTTACAGATTTCTTTAAAACTGAATTCAGTGAAGAAATATTGAATTTGGA 505
 Qy 483 TCGCCTGTGAAGACTTCAAGAAATGCAAGGAACCTCAACAAATCATCTTAAAGCAAAAG 542
 Db 506 TAGCCTGTGAAGATTTCAAGATAAGCAAGGACCTCAACAAATTCACCTTTAAAGCAAAAG 565
 Qy 543 CAATCTATGAGAAATTCATTTCAGAAATGTCGCCCCCAAGAGGTTAAACATTGATTTTCATA 602
 Db 566 CAATATATGAGAAATTTTATACAGACTGATCCCCCAAGAGGTTAACCTTTGATTTGCACA 625
 Qy 603 C 603
 Db 626 C 626
 Search completed: August 20, 2004, 12:31:53
 Job time : 3160.02 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2004, 12:36:30 ; Search time 79 Seconds

(without alignments)
840.489 Million cell updates/sec

Title: US-09-894-749-4

Perfect score: 1214

Sequence: 1 MDMSLVPSQLNMCSKEKT.....SRSTYNDQDVKSDVAIWL 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_25Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1214	100.0	235	Aay97154	Murine re
2	1214	100.0	235	Aae25830	Murine re
3	1032	85.0	235	Aay97153	Human reg
4	1032	85.0	235	Aae25829	Human reg
5	1032	85.0	235	Aau10749	Human RGS
6	1032	85.0	235	Abp64801	Human pro
7	994	81.9	227	Abp64054	Human ORF
8	429.5	35.4	211	ABP96779	Human COP
9	429.5	35.4	211	ABP98020	Amino aci
10	429.5	35.4	211	AD014019	Human src
11	429.5	35.4	220	Aab56929	Human pro
12	427.5	35.2	181	Aaw62075	Human reg
13	427.5	35.2	181	Aay53391	A human r
14	427.5	35.2	190	ABP62144	Human sec
15	412.5	34.0	181	ABP62144	Human sec
16	410	33.8	198	ABP62187	Rat disea
17	407.5	33.6	180	ABP62187	Human RGS
18	407.5	33.6	180	ABP62187	Human RGS
19	397.5	32.7	205	ABP62187	Human RGS
20	397.5	32.7	205	ABP62187	Human RGS
21	397.5	32.7	205	ABP62187	Human RGS
22	396	32.6	930	ABP62187	Human RGS
23	395.5	32.6	205	ABP62187	Human RGS
24	395.5	32.6	205	ABP62187	Human RGS
25	388	32.0	135	ABP98021	Amino aci

26	388	32.0	152	4	AAG66509	RGS prote
27	383	31.5	519	4	AAB90786	Human she
28	383	31.5	519	6	ABP99466	Amino aci
29	383	31.5	917	6	ADA13333	Human int
30	380	31.3	284	6	ADA54082	Human pro
31	375.5	30.9	923	6	ABU54617	Human NOV
32	374	30.8	118	2	AAY41001	Mouse RGS
33	369	30.4	116	2	AAY41020	RGS2 prot
34	364	30.0	202	2	AAR9895	PS3 respo
35	364	30.0	202	6	ABR92146	Human cer
36	363	29.9	202	2	AAW08133	Human cyt
37	363	29.9	202	2	AAW59294	Human RGS
38	363	29.9	202	3	AAY87952	Human CR1
39	362	29.8	81	5	AAU10747	Amino aci
40	360	29.7	128	7	ABR92620	Rat RGS4
41	360	29.7	167	5	AAU11043	Rat RGS4
42	356	29.3	201	2	AAW59293	Mouse RAT
43	353.5	29.1	249	6	ABP98019	Amino aci
44	350	28.8	111	6	ABP60081	Human RGS
45	347.5	28.6	196	4	AAB76863	Human lun

ALIGNMENTS

RESULT 1

AAy97154

ID AAY97154 standard; protein; 235 AA.

AC AAY97154;

XX 04-DEC-2000 (first entry)

DE Murine regulator of G-protein signaling protein.

XX RGS; regulators of G-protein signaling; GTPase activating protein; GAP;

KW G-alpha protein; cell adhesion; chemotaxis; vulnerability; immunosuppressor;

KW anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;

KW cytosolic; hepatotropic; anti-anemic; modulator; gene therapy.

OS Mus sp.

XX Key Location/Qualifiers

FT Domain 82..201

FT Misc-difference 83 /label= RGS_domain

FT Misc-difference 90 /note= "forms part of hydrophobic core"

FT Misc-difference 100 /note= "forms part of hydrophobic core"

FT Misc-difference 103 /note= "forms part of hydrophobic core"

FT Misc-difference 104 /note= "forms part of hydrophobic core"

FT Misc-difference 107 /note= "forms part of hydrophobic core"

FT Misc-difference 109 /note= "Makes direct contact with G-alpha-i"

FT Misc-difference 111 /note= "Makes direct contact with G-alpha-i"

FT Misc-difference 112 /note= "Makes direct contact with G-alpha-i"

FT Misc-difference 115 /note= "forms part of hydrophobic core"

FT Misc-difference 116 /note= "forms part of hydrophobic core"

FT Misc-difference 138 /note= "forms part of hydrophobic core"

FT Misc-difference 139 /note= "forms part of hydrophobic core"

FT Misc-difference 142 /note= "forms part of hydrophobic core"

FT Misc-difference 142 /note= "forms part of hydrophobic core"

Misc-difference 143 /note= "forms part of hydrophobic core"
 Misc-difference 151 /note= "forms part of hydrophobic core"
 Misc-difference 152 /note= "Makes direct contact with G-alpha-i"
 Misc-difference 154 /note= "Makes direct contact with G-alpha-i"
 Misc-difference 183 /note= "Makes direct contact with G-alpha-i"
 Misc-difference 184 /note= "forms part of hydrophobic core"
 Misc-difference 187 /note= "Makes direct contact with G-alpha-i"
 Misc-difference 188 /note= "Makes direct contact with G-alpha-i"
 Misc-difference 189 /note= "forms part of hydrophobic core"
 Misc-difference 191 /note= "Makes direct contact with G-alpha-i"
 Misc-difference 192 /note= "forms part of hydrophobic core"
 Misc-difference 193 /note= "forms part of hydrophobic core"
 Misc-difference 198 /note= "forms part of hydrophobic core"
 WO2000046236-A2.
 10-AUG-2000.
 04-FEB-2000; 2000WO-US002977.
 04-FEB-1999; 99US-00244314.
 (MILL-) MILLENNIUM PHARM INC.
 Hodge MR, Yowe D;
 WPI; 2000-532893/48.
 N-PSDB; AAA52090.
 Novel regulator of G-protein signaling nucleic acids and polypeptides,
 useful as diagnostic and investigative tools and to treat G-protein
 signaling disorders.
 Claim 8; Page 104; 105pp; English.
 The RGS (regulators of G-protein signaling) protein genes, clones
 AAH16395 and m1975, were identified in human and murine spleen cDNA
 libraries, respectively. Both proteins have unique N- and C-terminal
 sequences. The C-terminal location of the RGS domain is consistent with
 RGSs known to act as GTPase activating proteins (GAPs) for G-alpha
 proteins. G-alpha-1 linked receptors support rapid adhesion and directed
 migration of leukocytes and other cell types. The novel RGS proteins may
 be used to modulate cell adhesion and chemotaxis, e.g. for aiding wound
 repair. The RGS proteins, related cDNAs and anti-RGS antibodies are
 useful for modulation, diagnosis and treatment of immune and respiratory
 disorders
 Query Match 100.0%; Score 1214; DB 3; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1e-107;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MMSLVFFSOLNMCSEKTEFFKLMHSGCKETSIEAKIRAKENRLLSLQRPDFHGE 60
 1 MMSLVFFSOLNMCSEKTEFFKLMHSGCKETSIEAKIRAKENRLLSLQRPDFHGE 60
 61 TQASRALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFLKTFESENIEFWACE 120
 61 TQASRALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFLKTFESENIEFWACE 120

QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQPTLHSDFTQSRV 180
 DB 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQPTLHSDFTQSRV 180
 QY 181 YOLMEHDSYKRFILKSETYLHLIEGRPORPTNLRSSRSFTYNDQDKSDVAIWL 235
 DB 181 YOLMEHDSYKRFILKSETYLHLIEGRPORPTNLRSSRSFTYNDQDKSDVAIWL 235
 RESULT 2
 AAE25830
 ID AAE25830 standard; protein; 235 AA.
 AC AAE25830;
 DT 15-NOV-2002 (first entry)
 DE Murine regulator of G-protein signalling (RGS) protein, m1975.
 KW Murine; screening; RGS; regulator of G-protein signalling; pancreatitis;
 KW inflammatory disorder; allergy; Grave's disease; arthritis; sinusitis;
 KW respiratory disorder; asthma; pneumonia; therapy; immune disorder;
 KW haematological disorder; haematopoiesis; platelet-associated disorder;
 KW thrombocytopaenia; migration; invasive disorder; leukaemia; anaemia;
 KW erythrocyte-associated disorder; hepatitis; m1975.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT Domain 82..201
 FT /note= "RGS domain"
 FN US6410240-B1.
 FD 25-JUN-2002.
 FX 04-FEB-2000; 2000US-00498959.
 PR 04-FEB-1999; 99US-00244314.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Hodge MR, Yowe D;
 DR WPI; 2002-588886/63.
 DR N-PSDB; AAD42498.
 Screening assays for identifying agent that binds to human or mouse RGS
 (regulators of G-protein signaling) protein or its variant, or RGS
 protein encoded by homologous DNA sequences, or to host cell expressing
 the proteins.
 Claim 1; Col 57-60; 42pp; English.
 The invention relates to screening assays for identifying an agent that
 binds to: human or mouse RGS (regulators of G-protein signaling) protein
 or its variant, or RGS protein encoded by homologous DNA sequences; or a
 host cell expressing the RGS protein or its variant, or RGS protein
 encoded by homologous DNA sequences. The invention is useful for
 identifying an agent that binds to human or mouse RGS protein or its
 variant, or RGS protein encoded by homologous DNA sequences, or a host
 cell expressing the RGS protein or its variant, or RGS protein encoded by
 homologous DNA sequences. The agents identified using the invention are
 useful for modulating the activity of RGS proteins and thus useful for
 treating immune and inflammatory disorders (Grave's disease, allergy,
 arthritis), respiratory disorders (asthma, pneumonia, sinusitis),
 haematological disorders (haematopoiesis, migration), platelet-associated
 disorders (thrombocytopaenia), invasive disorders (leukaemia),
 erythrocyte-associated disorders (anaemia), pancreatitis, hepatitis etc.
 The present sequence is murine RGS protein, m1975
 Sequence 235 AA;
 QY
 DB
 QY
 DB

Query Match	100.0%;	Score 1214;	DB 5;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 1e-107;		
Matches 235;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MDMSLVFFSQINMCSEKKTFFKLMHGSGKETSIEAKIRAKENRNLISLLQRPDPHGE	60	
Db	1	MDMSLVFFSQINMCSEKKTFFKLMHGSGKETSIEAKIRAKENRNLISLLQRPDPHGE	60	
Qy	61	TOASRSALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACE	120	
Db	61	TOASRSALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACE	120	
Qy	121	DFKKCKEPOIILKAKIYEKIQNDAPKEVNIIDFHTKEVIAKSTAOPTLHSEFTAQSRV	180	
Db	121	DFKKCKEPOIILKAKIYEKIQNDAPKEVNIIDFHTKEVIAKSTAOPTLHSEFTAQSRV	180	
Qy	181	YQLMEHDSYKRFKSETYLHLIEGRPQPTNLRRRSRSTYNDFOVKSDVAIWL	235	
Db	181	YQLMEHDSYKRFKSETYLHLIEGRPQPTNLRRRSRSTYNDFOVKSDVAIWL	235	
RESULT 3				
AA97153	ID			
AA97153	standard; protein; 235 AA.			
XX	AC			
XX	AA97153;			
DT	04-DEC-2000	(first entry)		
XX	Human regulator of G-protein signaling protein.			
DE				
XX	RGS; regulators of G-protein signaling; GTPase activating protein; GAP;			
KW	G-alpha protein; cell adhesion; chemotaxis; vulnery; immunosuppressor;			
KW	anti-rheumatic; anti-arthritis; anti-diabetic; anti-inflammatory;			
KW	cytostatic; hepatotropic; anti-anaemic; modulator; gene therapy.			
XX	Homo sapiens.			
OS				
XX	Key			
PH	Location/Qualifiers			
FT	Domain	82..201		
FT	/label= RGS_domain			
FT	Misc-difference 83	/note= "forms part of hydrophobic core"		
FT	Misc-difference 90	/note= "forms part of hydrophobic core"		
FT	Misc-difference 100	/note= "forms part of hydrophobic core"		
FT	Misc-difference 103	/note= "forms part of hydrophobic core"		
FT	Misc-difference 104	/note= "forms part of hydrophobic core"		
FT	Misc-difference 107	/note= "forms part of hydrophobic core"		
FT	Misc-difference 109	/note= "Makes direct contact with G-alpha-i"		
FT	Misc-difference 111	/note= "Makes direct contact with G-alpha-i"		
FT	Misc-difference 112	/note= "Makes direct contact with G-alpha-i"		
FT	Misc-difference 115	/note= "Makes direct contact with G-alpha-i"		
FT	Misc-difference 116	/note= "forms part of hydrophobic core"		
FT	Misc-difference 138	/note= "forms part of hydrophobic core"		
FT	Misc-difference 139	/note= "forms part of hydrophobic core"		
FT	Misc-difference 142	/note= "forms part of hydrophobic core"		
FT	Misc-difference 143	/note= "forms part of hydrophobic core"		
FT	Misc-difference 151	/note= "forms part of hydrophobic core"		
FT				
FT	/note= "forms part of hydrophobic core"			
FT	/note= "Makes direct contact with G-alpha-i"			
FT	/note= "Makes direct contact with G-alpha-i"			
FT	/note= "forms part of hydrophobic core"			
FT	/note= "forms part of hydrophobic core"			
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FT	/note= "forms part of hydrophobic core"			
FT	/note= "forms part of hydrophobic core"			
FT	/			

Db 121 DFKSKGPOQIHLKAKAIYEKFIQTDPDAKEVNLDFHTKEVITNSIQPTLHSDFAAQRV 180
 QY 181 YQMEHDSYKRFKSTYHLIEGRPQPTNLRSSRSFTYNDQDVKSDVAIWL 235
 Db 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNEFDQVQSDVAIWL 235

RESULT 4
 ID AAE25829
 AC AAE25829
 XX
 DT 15-NOV-2002 (first entry)
 DE Human regulator of G-protein signalling (RGS) protein, h16395.
 XX Human; screening; RGS; regulator of G-protein signalling; pancreatitis;
 KW inflammatory disorder; allergy; Grave's disease; arthritis; sinusitis;
 KW respiratory disorder; asthma; pneumonia; therapy; immune disorder;
 KW haematological disorder; haematopoiesis; platelet-associated disorder;
 KW thrombocytopaenia; migration; invasive disorder; leukaemia; anaemia;
 KW erythrocyte-associated disorder; hepatitis; h16395.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 82..201
 FT /note= "RGS domain"
 XX
 PN US6410240-B1.
 XX
 PD 25-JUN-2002.
 XX
 PF 04-FEB-2000; 2000US-00498959.
 XX
 PR 04-FEB-1999; 99US-00244314.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Hodge MR, Yowe D;
 XX
 DR WPI; 2002-588886/63.
 DR N-PSDB; AAD42497.
 XX
 PT Screening assays for identifying agent that binds to human or mouse RGS
 PT (regulators of G-protein signaling) protein or its variant, or RGS
 PT protein encoded by homologous DNA sequences, or to host cell expressing
 PT the proteins.
 XX
 Claim 1; Col 55-56; 42pp; English.
 XX
 CC The invention relates to screening assays for identifying an agent that
 CC binds to: human or mouse RGS (regulators of G-protein signalling) protein
 CC or its variant, or RGS protein encoded by homologous DNA sequences; or a
 CC host cell expressing the RGS protein or its variant, or RGS protein
 CC encoded by homologous DNA sequences. The invention is useful for
 CC identifying an agent that binds to human or mouse RGS protein or its
 CC variant, or RGS protein encoded by homologous DNA sequences, or a host
 CC cell expressing the RGS protein or its variant, or RGS protein encoded by
 CC homologous DNA sequences. The agents identified using the invention are
 CC useful for modulating the activity of RGS proteins and thus useful for
 CC treating immune and inflammatory disorders (Grave's disease, allergy,
 CC arthritis), respiratory disorders (asthma, pneumonia, sinusitis),
 CC haematological disorders (haematopoiesis, migration), platelet-associated
 CC disorders (thrombocytopaenia), invasive disorders (leukaemia),
 CC erythrocyte-associated disorders (anaemia), pancreatitis, hepatitis etc.
 CC The present sequence is human RGS protein, h16395
 XX
 SQ Sequence 235 AA;
 Query Match 85.0%; Score 1032; DB 5; Length 235;
 Best Local Similarity 83.8%; Pred. No. 2.7e-90;

Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
 QY 1 MDMSLVFFSQNNMCSKEKTFKLMHSGSKEETSIEAKIRAKEKRNRLSLLQRPDPHGE 60
 Db 1 MEITLLFFSQNNMCSKEKTFKLIHSGSKEETSIEAKIRAKEKRNRLSLLVQKPEFHD 60
 QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTPLKTEFSEENIEFWACE 120
 Db 61 TRSRSGHLAKETRVSPPEAVKWAESFDKLLSHRDGLEAFTPLKTEFSEENIEFWACE 120
 QY 121 DFKKCKEPOQIHLKAKAIYEKFIQTDPDAKEVNLDFHTKEVITNSIQPTLHSDFAAQRV 180
 Db 121 DFKKSKGPOQIHLKAKAIYEKFIQTDPDAKEVNLDFHTKEVITNSIQPTLHSDFAAQRV 180
 QY 181 YQMEHDSYKRFKSTYHLIEGRPQPTNLRSSRSFTYNDQDVKSDVAIWL 235
 Db 181 YQMEQDSYTRFLKSDIYLDLMEGRPQPTNLRSSRSFTCNEFDQVQSDVAIWL 235

RESULT 5
 ID AAU10749 standard; protein; 235 AA.
 XX
 AC AAU10749;
 XX
 DT 12-MAR-2002 (first entry)
 DE Human RGS18 polypeptide.
 XX
 KW Human; regulator of G protein signalling; RGS18; arterial thrombosis;
 KW platelet activation dysfunction; myocardial infarction; stroke;
 KW coronary artery disease; cerebrovascular disease; unstable angina;
 KW deep vein thrombosis; systemic thromboembolism; anti-coagulant;
 KW invasive cardiac procedure.
 XX
 OS Homo sapiens.
 XX
 PN WO200183514-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 26-APR-2001; 2001WO-US013540.
 XX
 PR 28-APR-2000; 2000US-0200786P.
 PR 02-AUG-2000; 2000GB-00018833.
 XX
 PA (AVET) AVENTIS PHARM PROD INC.
 XX
 PI Murray DL, Gagnon AW;
 XX
 DR WPI; 2002-055453/07.
 DR N-PSDB; AAS18340.
 XX
 PT Isolated regulator of G protein signalling polypeptide, useful for
 PT prevention/treatment of platelet activation dysfunction, such as arterial
 PT thrombosis, myocardial infarction, coronary artery disease and stroke.
 XX
 Claim 31; Fig 1; 127pp; English.
 XX
 CC The present invention relates to the isolation of polynucleotide
 CC sequences that encode a novel regulator of G protein signalling (RGS)
 CC polypeptide, RGS18, from human platelets. The invention also provides
 CC nucleotide primers and probes specific for an RGS18 nucleic acid. The
 CC sequences of the invention are useful for the manufacture of a medicament
 CC for the prevention or treatment of a platelet activation dysfunction,
 CC such as arterial thrombosis, myocardial infarction, coronary artery
 CC disease, stroke, cerebrovascular disease, unstable angina, deep vein
 CC thrombosis, systemic thromboembolism, and in invasive cardiac procedures
 CC for anti-coagulant purposes. The sequences of the invention can also be
 CC used for the detection of RGS18 nucleic acids and RGS18 polypeptides. The
 CC present sequence represents the RGS18 polypeptide isolated from human
 CC platelets
 XX

CC	(ZSTs) for identifying expressed genes or for physical mapping of the
CC	human genome. The proteins may be used as molecular weight markers, or as
CC	nutritional sources or supplements. The proteins may be used to maintain
CC	and expand cell population in a totipotent or pluripotential state
CC	useful for re-engineering damaged or diseased tissues, transplantation,
CC	manufacture of bio-pharmaceuticals or the development of bio-sensors. The
CC	polynucleotides and proteins are useful for preventing, treating or
CC	ameliorating disorders involving aberrant protein expression or
CC	biological activity, e.g. haematopoietic disorders, central/peripheral
CC	nervous system diseases, mechanical and traumatic disorders, non-healing
CC	wounds, immune deficiencies and disorders, infectious diseases caused by
CC	viral, bacterial or fungal infection, autoimmune disorders, allergic
CC	reactions and conditions, coagulation disorders, or cancer. The
CC	polynucleotide sequences of the invention were assembled from ESTs
CC	isolated mainly by sequencing by hybridisation, and in some cases,
CC	sequences obtained from one or more public databases. Note: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 235 AA;
XX	
XX	Query Match 95.0%; Score 1032; DB 5; Length 235; .
XX	Best Local Similarity 83.8%; Pred. No. 2.7e-90;
XX	Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
XX	
QY	1 MDMSLFFPSOLNWCESKEKTFKLMGSGKEETSIAKIRAKERNFLSLLOQDPHGE 60
DB	1 METTLUFFSQINWCESKEKTFKLMGSGKEETSKEAKIRAKERNFLSLVQKPEPHD 60
QY	61 TQASRALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWVACE 120
DB	61 TRSSRSGLAKETRVSPEEAVKWAESFDKLLSHRDGLEAFTFLKTEFSEENIEFWIACE 120
QY	121 DFKCKEPPQIILKAKAIYEKFTQNDAPKEVNIDFHTKEVIKSIAGPTLHSPDTAOSRV 180
DB	121 DFKKSGPQOIHLKAKAIYEKFTQNDAPKEVNIDFHTKEVITNSITQTLHSPDAAOSRV 180
QY	181 YQLMEHDSYKRFKLSYTLHLIEGRPORPTNLRRRSRFTYNDPQDKSDVAIWL 235
DB	181 YQLMEQDSYTRFLKSDIYLLDMGRPQPTNLRRRSRFTYNDPQDKSDVAIWL 235
XX	
XX	RESULT 7
XX	ABP64054
XX	ABP64054 standard; protein; 227 AA.
XX	ABP64054;
XX	
DT	04-NOV-2002 (first entry)
DE	Human ORF424.
XX	
KW	Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary;
KW	Antiinflammatory; gene therapy; human; ORPX; atherosenic; platelet;
KW	human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;
KW	cancer; cardiovascular disease; allergy; autoimmune disease;
XX	wound healing; blood coagulation disorder; inflammatory disorder.
XX	
OS	Homo sapiens.
XX	
XX	US2002082206-A1.
PN	
XX	
PD	27-JUN-2002.
XX	
PF	30-MAY-2001; 2001US-00867550.
XX	
PR	30-MAY-2000; 2000US-0208427P.
XX	
XX	(LEAC/) LEACH M D.
PA	(MEHR/) MEHRABAN F.
PA	(CONL/) CONLEY P B.
PA	(TOPP/) TOPPER J N.

PI Koehler RH;
 XX WPI; 2003-278547/27.
 XX
 XX New polynucleotide encoding a regulator polypeptide of G-protein
 PT signaling (RGS) and RGS protein, useful in gene therapy to modulate the
 PT activity of RGS in a disease, particularly in asthma or diabetes.
 XX
 XX Disclosure; Fig 3; 99pp; English.
 XX
 CC The present sequence is a human regulator polypeptide of G-protein
 CC signaling (RGS) 2. The RGS gene is located on chromosome 1. The RGS
 CC polynucleotide and polypeptide are useful for identifying test compounds,
 CC that may act as agonists or antagonists at the receptor site and which
 CC can be regulated to provide therapeutic effects. The polynucleotide,
 CC polypeptide or vectors comprising the polynucleotide, and the reagents
 CC are useful for modulating the activity of RGS in a disease, particularly
 CC in asthma or diabetes
 XX
 SQ Sequence 211 AA;
 Query Match 35.4%; Score 429.5; DB 6; Length 211;
 Best Local Similarity 44.3%; Pred. No. 9.7e-33;
 Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;
 QY 4 SLVFFSOLNMCSKKTFFKLMHSGKETSIEAKIR--AKEKRNRLSLLQRPDPHGE 60
 DB 3 SAMFLAVQHDQRPMDKS-----AGSGHKSEKREKWKTLTKDWKTRLSYFLQNSSTPGK 57
 QY 61 TOARSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFLKTFESENIEFWVACE 120
 DB 58 PRTGKSKQQAIFKPSPEEAQLWSEAFDELLASKYGLAAFLKSEFCSENIETFWLACE 117
 QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQAQPTLHSEFTAQSRV 180
 DB 118 DFKTKSPQKLSKARKIYTDIEKAPKEINIDFQTKLIAQNIQEAATSGCFTTAQRV 177
 QY 181 YOLMEHDSYKRFKSETYLHLIEGRPORPT 210
 DB 178 YSLMNNYSYPRFLESEFYQDLCK-KPQITT 206
 RESULT 10
 ID ADD14019 standard; protein; 211 AA.
 AC ADD14019;
 DT 01-JAN-2004 (first entry)
 DE Human src biomarker polypeptide SEQ ID NO:208.
 KW predictor set; protein tyrosine kinase activity modulator;
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cytoskeletal;
 KW gene therapy; drug sensitivity; genetic profile; cancer; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2003062395-A2.
 XX 31-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-US001981.
 XX
 PR 18-JAN-2002; 2002US-0350061P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Huang F, Fairchild CR, Lee FY, Shaw P;
 XX WPI; 2003-636735/60.
 DR N-PSDB; ADD14613.
 XX

PT New polynucleotides and polypeptides for predicting the activity of
 PT compounds that interact with protein tyrosine kinases and/or protein
 XX tyrosine kinase pathways.
 XX
 XX Claim 10; SEQ ID NO 208; 139pp; English.
 XX
 CC The present invention describes a predictor set comprising a plurality of
 CC polynucleotides or polypeptides whose expression pattern is predictive of
 CC the response of cells to treatment with a compound that modulates protein
 CC tyrosine kinase activity or members of the protein tyrosine kinase
 CC pathway. Also described: (1) predicting whether a compound is capable of
 CC modulating the activity of cells, comprising obtaining a sample of cells,
 CC determining whether the cells express a plurality of markers, and
 CC correlating the expression of the markers to the compound's ability to
 CC modulate the activity of the cells; (2) a plurality of cell lines for
 CC identifying polynucleotides and polypeptides whose expression levels
 CC correlate with compound sensitivity or resistance of cells associated
 CC with a disease state; and (3) identifying polynucleotides and
 CC polypeptides that predict compound sensitivity or resistance of cells
 CC associated with a disease state, comprising subjecting the plurality of
 CC cell lines to one or more compounds, analysing the expression pattern of
 CC a microarray of polynucleotides or polypeptides, and selecting
 CC polynucleotides or polypeptides that predict the sensitivity or
 CC resistance of cells associated with a disease state by using the
 CC expression pattern of the microarray. The polynucleotides and
 CC polypeptides have cytostatic activities, and can be used in gene therapy.
 CC The polynucleotides and polypeptides are useful in predicting the
 CC activity of compounds that interact with protein tyrosine kinases and/or
 CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC genetic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 211 AA;
 Query Match 35.4%; Score 429.5; DB 7; Length 211;
 Best Local Similarity 44.3%; Pred. No. 9.7e-33;
 Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;
 QY 4 SLVFFSOLNMCSKKTFFKLMHSGKETSIEAKIR--AKEKRNRLSLLQRPDPHGE 60
 DB 3 SAMFLAVQHDQRPMDKS-----AGSGHKSEKREKWKTLTKDWKTRLSYFLQNSSTPGK 57
 QY 61 TOARSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFLKTFESENIEFWVACE 120
 DB 58 PRTGKSKQQAIFKPSPEEAQLWSEAFDELLASKYGLAAFLKSEFCSENIETFWLACE 117
 QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQAQPTLHSEFTAQSRV 180
 DB 118 DFKTKSPQKLSKARKIYTDIEKAPKEINIDFQTKLIAQNIQEAATSGCFTTAQRV 177
 QY 181 YOLMEHDSYKRFKSETYLHLIEGRPORPT 210
 DB 178 YSLMNNYSYPRFLESEFYQDLCK-KPQITT 206
 RESULT 11
 AAB56929
 ID AAB56929 standard; protein; 220 AA.
 XX
 XX AAB56929;
 AC AAB56929;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1507.
 XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardiactive; immunomodulatory; muscular;
 KW vulnary; gastrointestinal; nephrotropic; antiinfective; synaectological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.

XX OS Homo sapiens.
 XX PN WO200055174-A1.
 XX PD 21-SEP-2000.
 XX PF 08-MAR-2000; 2000WO-US005988.
 XX PR 12-MAR-1999; 99US-0124270P.
 XX PX (HUMA-) HUMAN GENOME SCI INC.
 XX PA (ROSE/) ROSEN C A.
 XX PI Rosen CA, Ruben SM;
 XX PX WPI: 2000-587513/55.
 XX DR N-PSDB; AAF16132.
 XX PT Prostate cancer associated gene sequences, referred to as prostate cancer
 PT PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT PT such as prostate cancer.
 XX PS Claim 11; Page 1946-1947; 2338pp; English.
 XX CC AAF15566 to AAF16505 encode the human prostate cancer associated
 CC CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC CC The prostate cancer antigens can have neuroprotective, cytoskeletal,
 CC CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CC CC and can be used in gene therapy. The prostate cancer antigen
 CC CC polynucleotides may be used for detection of prostate cancer. Chromosome
 CC CC identification, as chromosome markers, and for numerous other diagnostic
 CC CC or research purposes. The prostate cancer antigens may be used to treat
 CC CC disorders such as neural, immune, muscular, reproductive,
 CC CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC CC AAB57303 represent sequences used in the exemplification of the present
 CC CC invention
 XX CC Sequence 220 AA;
 Query Match 35.4%; Score 429.5; DB 3; Length 220;
 Best Local Similarity 44.3%; Pred. No. 1e-32;
 Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;
 QY 4 SLVFFSOLNMCSEKRTFFKLMHSGSKETSTEAKIR---AKEKENRLSLLLQRPDPFHGE 60
 DB 12 SAMFLAVQHDRCRPMDS-----AGSGHKSEKREKMKKRTLLKDWKTRLSYFLQNSSTFGK 66
 QY 61 TQASRSALLAKETRVSPPEAVKWSFQKLLSHRDGVDVAFTRFLKTEFSEENIEFWACE 120
 DB 67 PXTGKSKQQAIFKSPPEAQWSEAFDELLASKYGLAAFAFLAKSECEENIEFWACE 126
 QY 121 DPKCKEPOQIILKAKAIVEKFIQNDAPKEVNIDPHTEKVIKSTIAQPTLHSFDTAQSRV 180
 DB 127 DPKTKSPQKLSKARKIYTDPIEKEAPKEINIDPQTTLIAQNIQETSGCFTTAQKRV 186
 QY 181 YQLMEHDSYKRFKSTYLLHLIEGRPQPT 210
 DB 187 YSLMENNIPRFLSEFYOQLCK-KPQITT 215
 RESULT 12
 ID AAW62075
 AA AAW62075 standard; protein; 181 AA.
 AC AAW62075;
 XX 14-SEP-1998 (first entry)
 DT Human regulator of G-protein signalling.
 DE
 XX

KW Human; regulator; G-protein signalling; HRGS; cancer; inflammation;
 KW hypertension; cardiovascular shock; arrhythmias; asthma.
 OS Homo sapiens.
 XX WO9820128-A1.
 XX PD 14-MAY-1998.
 XX PF 06-NOV-1997; 97WO-US018476.
 XX PR 08-NOV-1996; 96US-00748483.
 XX PX (INCY-) INCYTE PHARM INC.
 XX PA Hillman JL, Goli SK;
 XX PI WPI: 1998-286944/25.
 XX DR N-PSDB; AAV38084.
 XX PT Regulator of G-protein signalling - used to develop products for treating
 PT PT e.g. cancer, inflammation, hypertension, cardiovascular shock,
 PT PT arrhythmias or asthma.
 XX PS Claim 1; Fig 1; 66pp; English.
 XX CC The present sequence represents human regulator of G-protein signalling
 CC CC (HRGS). The HRGS regulates G-protein signalling in cancer cells and may
 CC CC be useful in the treatment of any cancer, especially cancers of the brain
 CC CC and thyroid. Products of the present invention can also be used for
 CC CC treating other conditions associated with uncontrolled cell signalling
 CC CC such as inflammation. The products can also be used to modulate HRGS
 CC CC activity in response to disorders involving the sympathetic nervous
 CC CC system including hypertension, cardiovascular shock, arrhythmias and
 CC CC asthma. The products can also be used for detection, diagnosis and drug
 CC CC screening
 XX CC Sequence 181 AA;
 Query Match 35.2%; Score 427.5; DB 2; Length 181;
 Best Local Similarity 50.3%; Pred. No. 1.2e-32;
 Matches 84; Conservative 33; Mismatches 47; Indels 3; Gaps 1;
 QY 40 RAKEKRNRLSLLLQRPDPFHGE---TQASRSALLAKETRVSPPEAVKWSFQKLLSHRDG 96
 DB 15 RAKEIKIKILLQKQDSVGDVLPYNEXPEKPAKTQKTSLEALQWRDSDLKLLQNNYG 74
 QY 97 VDAFTPLKTEFSEENIEFWACEDEKCKEPOQIILKAKAIVEKFIQNDAPKEVNIDPH 156
 DB 75 LASFKSFLKSEFSEENLEFWACEDYKTKRSPANMAEKAKQIYEEFIQTEAPKEVNIDPH 134
 QY 157 TKEVIKSTIAQPTLHSFDTAQSRVYQIMBHDSYKRFKSETYLLHLIE 203
 DB 135 TKDITKMLVEPSLSFSDVAQKEIHALMEKDSLPFRVSEFYQELIK 181
 RESULT 13
 ID AAY53931
 AA AAY53931 standard; protein; 181 AA.
 AC AAY53931;
 XX 13-MAR-2000 (first entry)
 DT A human regulator of G protein signalling RG85 protein.
 DE
 XX Activator of G protein signalling; AGS; ras-related G protein;
 XX GTP hydrolysis; G protein activity; pheromone response pathway;
 XX G protein-coupled signal transduction; G-gamma selectivity;
 XX cellular signal transduction; regulator of G protein signalling; RG85.
 XX Homo sapiens.
 XX

```

PN WO958670-A1.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-US010151.
XX
PR 08-MAY-1998; 98US-0084842P.
XX
PR 07-OCT-1998; 98US-0103355P.
XX
PA (CADU-) CADUS PHARM CORP.
XX
PI Cismowski M, Duzic E;
XX
DR WPI: 2000-072337/06.
XX
DR N-PSDB; AA236910.
XX
XX
PT A new activator of G protein signalling used to treat disorders
PT characterized by an aberrant AGS protein activity.
XX
XX Claim 74; Page 141-141; 162pp; English.
XX
XX The present sequence represents a regulator of G protein signalling (AGS)
CC protein, RGS5. The specification also describes an activator of G protein
CC signalling (AGS) protein. The AGS cDNA sequence was isolated from a human
CC liver cDNA library. The AGS protein exhibits homology to ras-related G
CC proteins, and contains alterations in conserved amino acids consistent
CC with a deficiency in GTP hydrolysis activity. AGS stimulates G protein
CC activity, G protein-coupled signal transduction and the pheromone
CC response pathway in a receptor-independent manner. The AGS protein also
CC shows G-gamma selectivity, as measured by growth assays in yeast
CC expressing various mammalian G-gamma constructs, and tissue-specific
CC expression, as measured by Northern blot analysis. The AGS protein can be
CC used to screen for compounds that modulate cellular signal transduction.
CC The protein is used to treat disorders characterized by an aberrant AGS
CC protein activity or AGS nucleic acid expression
XX
XX Sequence 181 AA;

Query Match 35.2%; Score 427.5; DB 3; Length 181;
Best Local Similarity 50.3%; Pred. No. 1.2e-32;
Matches 84; Conservative 33; Mismatches 47; Indels 3; Gaps 1;

QY 40 RAKEKRNLSLLQRPDPHGE---TQASRSALLAKETRVSPPEAVKWAESFDKLSHRDG 96
DB 15 RAKEIKIKLILQKPSVGDVLPYNEKEPKAKTKTSLDEALQWRDSDLKLQNNYG 74
QY 97 VDAFTRFLKTEFSEENIEFWACEDFKCKEPOQIILKAKIYKFIQNDAPKEVNIDFH 156
DB 75 LASFKSFLKSEFSEENLEFWIACEDYKKIKSPAKWAERAKQIYEEFIQTEAPKEVNIDHF 134
QY 157 TKEVIATKSTAOPTLHSFDTAQSRVYQVLMHDSYKRFKLSYTLHLIE 203
DB 135 TKDITMKNLVEPSLSSFDMAQKRIHALMEKDSLPRFVRSEFYQELIK 181

RESULT 14
ABP62144
ID ABP62144 standard; protein; 190 AA.
XX
XX ABP62144;
XX
XX 12-NOV-2002 (first entry)
XX
XX Human secreted protein SEQ ID NO 197.
XX
XX Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
XX immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
XX antiparkinsonian; antisickling; antianemic; antiarthritic; cancer;
XX antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
XX

```

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OS Homo sapiens.
XX
PN WO200257420-A2.
XX
PD 25-JUL-2002.
XX
PF 17-JAN-2002; 2002WO-US001109.
XX
PR 18-JAN-2001; 2001US-0262066P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen CA, Olsen H;
PI Ebner R, Brewer LA;
XX
XX WPI: 2002-599716/64.
XX
XX New polynucleotides and polypeptides useful for diagnosing, prognosing,
PT treating or preventing e.g. neurodegenerative, central nervous system,
PT autoimmune, respiratory, reproductive, or inflammatory diseases or
PT disorders.
XX
XX Claim 11; Page 71; 785pp; English.
XX
XX The invention relates to novel genes (ABQ92553-ABQ92607) and proteins
CC (ABP62013-ABP62153) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections
XX
XX Sequence 190 AA;

Query Match 35.2%; Score 427.5; DB 5; Length 190;
Best Local Similarity 50.3%; Pred. No. 1.3e-32;
Matches 84; Conservative 33; Mismatches 47; Indels 3; Gaps 1;

QY 40 RAKEKRNLSLLQRPDPHGE---TQASRSALLAKETRVSPPEAVKWAESFDKLSHRDG 96
DB 24 RAKEIKIKLILQKPSVGDVLPYNEKEPKAKTKTSLDEALQWRDSDLKLQNNYG 83
QY 97 VDAFTRFLKTEFSEENIEFWACEDFKCKEPOQIILKAKIYKFIQNDAPKEVNIDFH 156
DB 84 LASFKSFLKSEFSEENLEFWIACEDYKKIKSPAKWAERAKQIYEEFIQTEAPKEVNIDHF 143
QY 157 TKEVIATKSTAOPTLHSFDTAQSRVYQVLMHDSYKRFKLSYTLHLIE 203
DB 144 TKDITMKNLVEPSLSSFDMAQKRIHALMEKDSLPRFVRSEFYQELIK 190

RESULT 15
ABB83788
ID ABB83788 standard; protein; 181 AA.
XX
XX ABB83788;
XX
XX 14-AUG-2002 (first entry)
XX
XX Rat disease associated protein SEQ ID NO 1.
XX
XX Rat; cardiant; heart disease; cardiovascular disease; cardiac infarction;
XX angina; gene therapy.
XX
XX Rattus sp.

```

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XX WO200233082-A1.
PN
XX
XX
PD 25-APR-2002.
XX
XX 18-OCT-2001; 2001WO-JF009140.
XX
XX 19-OCT-2000; 2000JP-00319912.
PR
XX 16-NOV-2000; 2000JP-00350183.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX Koyama N, Tanida S, Watanabe T;
PI
XX
XX WPI; 2002-394557/42.
DR
DR N-PSDB; ABL99975.
XX
XX Disease-associated gene and encoded RGSS-like protein, applicable in
PT diagnosis and prevention of treatment of heart diseases e.g.
PT cardiovascular diseases, cardiac infarction, heart failure and angina,
PT including gene therapy.
XX
PS Claim 1; Page 71-72; 82pp; Japanese.
XX
XX The invention relates to a protein (ABB83788) or its salt. The protein
CC and encoded DNA (ABL99975) are applicable in diagnosis and prevention or
CC treatment of heart diseases e.g. cardiovascular diseases, cardiac
CC infarction, heart failure and angina, including gene therapy
XX
SQ Sequence 181 AA;
Query Match 34.0%; Score 412.5; DB 5; Length 181;
Best Local Similarity 49.1%; Pred. No. 3.3e-31;
Matches 86; Conservative 27; Mismatches 41; Indels 21; Gaps 2;
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Db 15 RAKEIKIKIGILLQKPD-----SAVDLVIPIYNEKPEKPAKHKPSLEEVLQWRQSL 65
QY 88 DXLLSHRDGVDAFTPLKTEFSEENIEFWACEDFKCKEPCQIILKAKIYKFIQND 147
Db 66 DXLLQSNYGFASFKSFLKSEFSEENLEFWACENYKIKSPKMAEKAKQIYEEFIQTEA 125
QY 148 PREVNIDHTKEVIKASIAQPTLHSDTAQSRVYQVQIMEHDSYKRLKSETVLHLI 202
Db 126 PREVNIDHTKQITMKNLVEPSHSDLAQKRIYALMEKDSLPRFVRSEFYKELI 180

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Search completed: August 20, 2004, 16:44:15
Job time : 80 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2004, 16:40:58 ; Search time 18.5 Seconds
(without alignments)
655.789 Million cell updates/sec

Title: US-09-894-749-4
Perfect score: 1214
Sequence: 1 MDMSLVFSQLNMCSEKKT.....SRSTYNDFOVKSDVAIWL 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B-COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A-COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B-COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCTUS-COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1214	100.0	235	3	US-09-244-314-4
2	1214	100.0	235	4	US-09-498-959-4
3	1032	85.0	235	4	US-09-244-314-2
4	1032	85.0	235	4	US-09-498-959-2
5	429.5	35.4	211	2	US-08-748-483-4
6	427.5	35.2	181	2	US-08-748-483-1
7	397.5	32.7	205	2	US-08-829-110-6
8	397.5	32.7	205	2	US-08-748-483-5
9	370	30.5	120	4	US-08-890-865A-11
10	364	30.0	202	1	US-08-274-318-2
11	364	30.0	202	2	US-08-754-108-2
12	363	29.9	202	2	US-08-463-081B-2
13	363	29.9	202	2	US-08-461-379A-2
14	363	29.9	202	2	US-08-462-390B-2
15	363	29.9	202	3	US-08-870-815-4
16	363	29.9	202	3	US-08-463-074B-2
17	363	29.9	202	3	US-08-465-585C-2
18	363	29.9	202	3	US-08-652-446-2
19	363	29.9	202	3	US-08-949-004-4
20	359.5	29.6	121	2	US-08-588-258B-32
21	359.5	29.6	121	3	US-08-460-505-32
22	359.5	29.6	121	5	PCT-US96-08235-32
23	354	29.2	120	4	US-08-890-865A-12
24	348	28.7	201	2	US-08-890-865A-14
25	348	28.7	201	2	US-08-726-228-2
26	348	28.7	201	3	US-08-870-815-2
27	348	28.7	201	3	US-08-949-004-2

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Sequence 3, Appli
Sequence 339, App
Sequence 339, App
Sequence 339, App
Sequence 339, App
Sequence 339, App
Sequence 31, Appl
Sequence 31, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 13, Appl
Sequence 51, Appl
Sequence 1, Appl
Sequence 16, Appl
Sequence 3, Appl
Sequence 30, Appl
Sequence 30, Appl

28 347.5 28.6 196 2 US-08-829-110-5
29 347.5 28.6 196 2 US-08-748-483-3
30 347.5 28.6 196 4 US-09-702-705-339
31 347.5 28.6 196 4 US-09-736-457-339
32 347.5 28.6 196 4 US-09-614-124B-339
33 347.5 28.6 196 4 US-09-671-325-339
34 347.5 28.6 196 4 US-09-589-184-339
35 336.5 27.7 119 2 US-08-588-258B-31
36 336.5 27.7 119 3 US-08-460-505-31
37 336.5 27.7 119 5 PCT-US96-08295-31
38 334.5 27.6 119 4 US-08-890-865A-15
39 328 27.0 120 4 US-08-890-865A-13
40 307 25.3 217 4 US-09-976-594-51
41 303 25.0 159 2 US-08-829-110-1
42 284 23.4 120 4 US-08-890-865A-16
43 277.5 22.9 243 2 US-08-829-110-3
44 274.5 22.6 119 2 US-08-588-258B-30
45 274.5 22.6 119 3 US-08-460-505-30

ALIGNMENTS

RESULT 1
US-09-244-314-4
; Sequence 4, Application US/09244314
; Patent No. 6274362
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/244,314
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-244-314-4

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Best Local Similarity 100.0%; Pred. No. 2,1e-115;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDMSLVFSQLNMCSEKKTFFKLMHSGKEETSIEAKIRAKERNLSLLLPDPHGE 60

QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFLKTFESENIEFWVACE 120
Db 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFLKTFESENIEFWVACE 120

QY 121 DFKCKEPOQIILKAKAIYEKFIQNDAPKVDNDFHTKEVIKSIQFTLHSPDTASRV 180
Db 121 DFKCKEPOQIILKAKAIYEKFIQNDAPKVDNDFHTKEVIKSIQFTLHSPDTASRV 180

QY 181 YOLMEHSDYKRFKSEYTLHLIEGRPORPTNLRSSRSFTYNDFOVKSDVAIWL 235
Db 181 YOLMEHSDYKRFKSEYTLHLIEGRPORPTNLRSSRSFTYNDFOVKSDVAIWL 235

RESULT 2
US-09-498-959-4
; Sequence 4, Application US/09498959
; Patent No. 6410240
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses
; TITLE OF INVENTION: RGS-Containing Molecules and Uses
; FILE REFERENCE: 5800-19A

RESULT 4
US-09-498-959-2
; CURRENT APPLICATION NUMBER: US/09/498,959
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: 09/244,314
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-498-959-4

Query Match 100.0%; Score 1214; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.1e-115; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MDMSLVFFSQNNCESKEKTFKLMHSGKETSIEAKIRAKENRNLSSLLQRPDPHGE 60
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DB 61 TQASRGALLAKETRVSPEEAVKWAESFDKLLSHRDGVDFTFLKTEFSEENIEFWACE 120
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DB 121 DFKCKEPOQIILKAKAIYEKTIQNDAPKEVNIDFHTKEVIKASTIAQPTLHSFDTAQSRV 180
QY 181 YQMEHDSYKRFKLSYTHLIEGRPQRTNLRSSRSTYNDFOVQSDVAIWL 235
DB 181 YQMEHDSYKRFKLSYTHLIEGRPQRTNLRSSRSTYNDFOVQSDVAIWL 235

RESULT 3
US-09-244-314-2
; Sequence 2, Application US/092443.4
; Patent No. 6274362
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/244,314
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-314-2

Query Match 85.0%; Score 1032; DB 3; Length 235;
Best Local Similarity 83.8%; Pred. No. 6.3e-97; Indels 0; Gaps 0;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
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DB 61 TQASRGALLAKETRVSPEEAVKWAESFDKLLSHRDGVDFTFLKTEFSEENIEFWACE 120
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DB 121 DFKCKEPOQIILKAKAIYEKTIQNDAPKEVNIDFHTKEVIKASTIAQPTLHSFDTAQSRV 180
QY 181 YQMEHDSYKRFKLSYTHLIEGRPQRTNLRSSRSTYNDFOVQSDVAIWL 235
DB 181 YQMEHDSYKRFKLSYTHLIEGRPQRTNLRSSRSTYNDFOVQSDVAIWL 235

RESULT 4
US-09-498-959-2
; Sequence 2, Application US/09498959
; Patent No. 6410240
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 5800-19A
; CURRENT APPLICATION NUMBER: US/09/498,959
; CURRENT FILING DATE: 2000-02-04
; EARLIER APPLICATION NUMBER: 09/244,314
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-498-959-2

Query Match 85.0%; Score 1032; DB 4; Length 235;
Best Local Similarity 83.8%; Pred. No. 6.3e-97;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
QY 1 MDMSLVFFSQNNCESKEKTFKLMHSGKETSIEAKIRAKENRNLSSLLQRPDPHGE 60
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QY 61 TQASRGALLAKETRVSPEEAVKWAESFDKLLSHRDGVDFTFLKTEFSEENIEFWACE 120
DB 61 TQASRGALLAKETRVSPEEAVKWAESFDKLLSHRDGVDFTFLKTEFSEENIEFWACE 120
QY 121 DFKCKEPOQIILKAKAIYEKTIQNDAPKEVNIDFHTKEVIKASTIAQPTLHSFDTAQSRV 180
DB 121 DFKCKEPOQIILKAKAIYEKTIQNDAPKEVNIDFHTKEVIKASTIAQPTLHSFDTAQSRV 180
QY 181 YQMEHDSYKRFKLSYTHLIEGRPQRTNLRSSRSTYNDFOVQSDVAIWL 235
DB 181 YQMEHDSYKRFKLSYTHLIEGRPQRTNLRSSRSTYNDFOVQSDVAIWL 235

RESULT 5
US-08-748-483-4
; Sequence 4, Application US/08748483
; Patent No. 5955314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,483
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

```

;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 57362
;
; US-08-748-483-1
;
; Query Match 35.2%; Score 427.5; DB 2; Length 181;
; Best Local Similarity 50.3%; Pred. No. 1.1e-35;
; Matches 84; Conservative 33; Mismatches 47; Indels 3; Gaps 1
;
;
; QY 40 RAKEKRNLSLLQLRPDFHGE---TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDG 96
; Db 15 RAKETIKIKLIGLLQKPSDVGDLVIPYNEKPEKPAKTQKTSLDEALQWRDLSLKLQNNYG 74
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; QY 97 VDAFTRELKTFESSENTIEFWVACEDFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIIDFH 156
; Db 75 LASFSKSFUKSFSSENLEFWIACEDYAKIKSPAMAEKAKQIYEFTQTEAPKEVNIIDFH 134
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; QY 157 TREVIAXSIAQPTLHSEDTTAQSRVYQLMEHDSYKRELFKSETYIHLIE 203
; Db 135 TKDITMKNLVFPSSSFDMAQKRIHALMEKDSLPRFVRSFQELIK 181
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; RESULT 7
; US-08-829-110-6
; Sequence 6, Application US/08829110
; Patent No. 5882890
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
; TITLE OF INVENTION: SIGNALING
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,110
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0259 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank

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/ APPLICANT: Kley, Nikolai
/ TITLE OF INVENTION: No. 5867987el p53 Response Genes
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Bristol-Myers Squibb Company
/ STREET: 3005 First Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98121
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/274,318
/ FILING DATE: 11-JUL-1994
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bogden, James M.
/ REGISTRATION NUMBER: 32,962
/ REFERENCE/DOCKET NUMBER: ON0127-
/ TELEPHONE: 206-727-3688
/ TELEFAX: 206-727-3601
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 202 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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/ US-08-274-318-2
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/ Query Match 30.0%; Score 364; DB 1; Length 202;
/ Best Local Similarity 45.8%; Pred. No. 3.5e-29;
/ Matches 76; Conservative 29; Mismatches 57; Indels 4; Gaps 1;
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/ Db 75 GVAAFHAFHLKTFSESENIWFVACEDFKCKEPOQIILKAKAIYKFTQNDAPKEVNIDF 134
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/ RESULT 11
/ US-08-754-108-2
/ Sequence 2, Application US/08/754108
/ Patent No. 5886149
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/ GENERAL INFORMATION:
/ APPLICANT: Buckbinder, Leonard
/ APPLICANT: Talbott, Randy
/ APPLICANT: Seizinger, Bernd R.
/ APPLICANT: Kley, Nikolai
/ TITLE OF INVENTION: No. 5886149el p53 Response Genes
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Bristol-Myers Squibb Company
/ STREET: 3005 First Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98121
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/754,108
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/274,318
/ FILING DATE: 11-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bogden, James M.
/ REGISTRATION NUMBER: 32,962
/ REFERENCE/DOCKET NUMBER: ON0127-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-727-3688
/ TELEFAX: 206-727-3601
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 202 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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/ US-08-754-108-2
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/ Query Match 30.0%; Score 364; DB 2; Length 202;
/ Best Local Similarity 45.8%; Pred. No. 3.5e-29;
/ Matches 76; Conservative 29; Mismatches 57; Indels 4; Gaps 1;
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/ Qy 40 RAKEKRNLSLLQRPDPFHGET---QASRSALLAKETRVSPPEAVKWAESFDKLLSHRD 95
/ Db 15 RAKEFKTRLGIFLHKSELGCDTGSTGKSEWGSKHKNRNFSDVLGWRSEFDLLSSKN 74
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/ Qy 96 GVDATFRFLKTFSESENIWFVACEDFKCKEPOQIILKAKAIYKFTQNDAPKEVNIDF 155
/ Db 75 GVAAFHAFHLKTFSESENIWFVACEDFKCKEPOQIILKAKAIYKFTQNDAPKEVNIDH 134
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/ RESULT 12
/ US-08-463-081B-2
/ Sequence 2, Application US/08463081B
/ Patent No. 5871960
/ Patent No. 5871960 5837487
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/ GENERAL INFORMATION:
/ APPLICANT: Smith, Kendall A. & Beadling, Carol
/ TITLE OF INVENTION: Nucleic Acids Encoding CFS Polypeptide,
/ TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
/ STREET: 444 South Flower St. - Suite 1900
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90071
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0,
/ SOFTWARE: Version #1.25
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/463,081B
/ FILING DATE: 5-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/104,736
/ FILING DATE: 10-AUG-1993
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/796,066
/ FILING DATE: 20-NOV-91
/ ATTORNEY/AGENT INFORMATION:
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NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-081B-2

Query Match 29.9%; Score 363; DB 2; Length 202;
Best Local Similarity 45.8%; Pred. No. 4.5e-29;
Matches 76; Conservative 29; Mismatches 57; Indels 4; Gaps 1;

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Db 15 RAKEFKTRLGIFLHKSELGCDTGTGKFWGSKHSENFSEDVLGWRESFDLLSSKN 74

QY 96 GVDATFRFLKTERSEENIEFWACEDFKCKEPPQOIILKAKAIYEKFIQNDAPKEVNIDF 155
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; Sequence 2, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US8N 08/330,108; 08/104,736
; FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-070
; TELEPHONE: (610)470-0701
; TELEFAX: (610)470-0701
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear

QY 40 RAKEKRNRLSLIQRDPFHGETQASR-----SALLAKETRVSPPEAVKWAESFDKLLSHRD 95
Db 15 RAKEFKTRLGIFLHKSELGCDTGTGKFWGSKHSENFSEDVLGWRESFDLLSSKN 74

NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-081B-2

Query Match 29.9%; Score 363; DB 2; Length 202;
Best Local Similarity 45.8%; Pred. No. 4.5e-29;
Matches 76; Conservative 29; Mismatches 57; Indels 4; Gaps 1;

QY 40 RAKEKRNRLSLIQRDPFHGETQASR-----SALLAKETRVSPPEAVKWAESFDKLLSHRD 95
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QY 96 GVDATFRFLKTERSEENIEFWACEDFKCKEPPQOIILKAKAIYEKFIQNDAPKEVNIDF 155
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RESULT 14
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; Sequence 2, Application US/08462390B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A. & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,390B
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US8N 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US8N 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: US8N 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-040
; TELEPHONE: (610)407-0700
; TELEFAX: (610)407-0701
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-390B-2

Query Match 29.9%; Score 363; DB 2; Length 202;
Best Local Similarity 45.8%; Pred. No. 4.5e-29;
Matches 76; Conservative 29; Mismatches 57; Indels 4; Gaps 1;

QY 40 RAKEKRNRLSLIQRDPFHGETQASR-----SALLAKETRVSPPEAVKWAESFDKLLSHRD 95
Db 15 RAKEFKTRLGIFLHKSELGCDTGTGKFWGSKHSENFSEDVLGWRESFDLLSSKN 74

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2004, 16:47:08 ; Search time 239 Seconds

(without alignments)
308.996 Million cell updates/sec

Title: US-09-894-749-4

Perfect score: 1214

Sequence: 1 MDMSLVFSQLNMCSEKST.....SRSTYNDQVKSQDVAIWL 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
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2	1032	85.0	235	9	US-09-894-749-4
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4	994	81.9	227	9	US-09-867-550-848
5	429.5	35.4	211	9	US-09-206-639-4
6	429.5	35.4	211	12	US-10-258-371B-24
7	429.5	35.4	211	16	US-10-408-765A-493
8	429.5	35.4	220	9	US-09-925-300-1507
9	429.5	35.2	181	9	US-09-206-639-1
10	427.5	35.2	181	12	US-10-258-371B-22
11	427.5	35.2	190	14	US-10-411-224-197
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13	412.5	34.0	181	14	US-10-398-953-1
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16	397.5	32.7	205	9	US-09-206-639-5	Sequence 5, Appli
17	397.5	32.7	205	10	US-09-939-209A-2	Sequence 2, Appli
18	397.5	32.7	205	12	US-10-258-371B-21	Sequence 21, Appli
19	396	32.6	930	14	US-10-113-794A-1	Sequence 1, Appli
20	383	31.5	519	12	US-10-258-371B-28	Sequence 28, Appli
21	383	31.5	519	14	US-10-113-794A-2	Sequence 2, Appli
22	383	31.5	519	15	US-10-428-487-14	Sequence 14, Appli
23	383	31.5	591	15	US-10-108-260A-3970	Sequence 3970, Ap
24	381	31.4	776	12	US-10-087-192-1728	Sequence 1728, Ap
25	380	31.3	284	15	US-10-094-749-1650	Sequence 1650, Ap
26	375.5	30.9	923	12	US-10-114-270-152	Sequence 152, App
27	364	30.0	202	14	US-10-171-311-202	Sequence 202, App
28	363	29.9	202	9	US-09-873-438-4	Sequence 4, Appli
29	363	29.9	204	12	US-10-258-371B-23	Sequence 23, Appli
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38	347.5	28.6	196	9	US-09-849-626-339	Sequence 339, App
39	347.5	28.6	196	10	US-09-476-300-339	Sequence 339, App
40	347.5	28.6	196	12	US-10-283-017-339	Sequence 339, App
41	347.5	28.6	196	14	US-10-017-754-339	Sequence 339, App
42	347.5	28.6	196	14	US-10-113-872-339	Sequence 339, App
43	347.5	28.6	196	14	US-10-247-671-176	Sequence 176, App
44	347.5	28.6	217	9	US-09-925-301-1292	Sequence 1292, Ap
45	345.5	28.5	196	12	US-10-170-385-375	Sequence 375, App

ALIGNMENTS

RESULT 1

US-09-894-749-4
; Sequence 4, Application US/09894749
; Patent No. US20020081683A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5900-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/894,749
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/244,314
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-894-749-4

Query Match		100.0%;	Score 1214;	DB 9;	Length 235;
Best Local Similarity		100.0%;	Pred. No. 7.4e-110;		
Matches 235;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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; Sequence 2, Application US/09894749
; Patent No. US20020081683A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Yowe, David
; TITLE OF INVENTION: RGS-Containing Molecules and Uses Thereof
; FILE REFERENCE: 5800-19, 035800/174680
; CURRENT APPLICATION NUMBER: US/09/894, 749
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/244,314
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-894-749-2

Query Match      85.0%; Score 1032; DB 9; Length 235;
Best Local Similarity 83.8%; Pred. No. 3.9e-92;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

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US-10-258-371B-20
; Sequence 20, Application US/10258371B
; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Alison
; APPLICANT: MURRAY, David L
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
; FILE REFERENCE: A3656 US PCT
; CURRENT APPLICATION NUMBER: US/10/258, 371B
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: GB001883.334
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/200,786
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-371B-20

Query Match      85.0%; Score 1032; DB 12; Length 235;
Best Local Similarity 83.8%; Pred. No. 3.9e-92;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;
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Qy      1  MDMSLVFFSQINNCESKEKTFKLMHSGKETSIEAKIRAKEKRNRLSLLQRPDPFGE 60
Db      1  METTLFFSQINNCESKEKTFKLIHSGKETSKEAKIRAKEKRNRLSLLQKPEFHE 60
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Qy      61  TQASRSALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTRELKTEFSEENIEFWACE 120
Db      61  TRSSRSGLAKETRVSPEEAVKWAESFDKLLSHRDGLEAFTRELKTEFSEENIEFWACE 120
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Qy      121 DFKKCKEPOQIILKAKAIYEKFTQNDAPKEVNDFTKEVIKSIQPTLHSDTAQSRV 180
Db      121 DFKKSGKPGQIHLKAKAIYEKFTQNDAPKEVNDFTKEVITNSITQPTLHSDFAAQRV 180
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Qy      181 YQIMEHDSYKRFKSETYLHLIEGRPQPTNLRSSRSFTYNDQDVKSDVAIWL 235
Db      181 YQIMEQDSYTRFLKSDIYLDMEGRPQPTNLRSSRSFTCNCFQDVQSDVAIWL 235
|||||
RESULT 4
US-09-867-550-848
; Sequence 848, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and I
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-848

Query Match      81.9%; Score 994; DB 9; Length 227;
Best Local Similarity 83.7%; Pred. No. 1.9e-88;
Matches 190; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy      1  MDMSLVFFSQINNCESKEKTFKLMHSGKETSIEAKIRAKEKRNRLSLLQRPDPFGE 60
Db      1  METTLFFSQINNCESKEKTFKLIHSGKETSKEAKIRAKEKRNRLSLLQKPEFHE 60
|||||
Qy      61  TQASRSALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTRELKTEFSEENIEFWACE 120
Db      61  TRSSRSGLAKETRVSPEEAVKWAESFDKLLSHRDGLEAFTRELKTEFSEENIEFWACE 120
|||||
Qy      121 DFKKCKEPOQIILKAKAIYEKFTQNDAPKEVNDFTKEVIKSIQPTLHSDTAQSRV 180
Db      121 DFKKSGKPGQIHLKAKAIYEKFTQNDAPKEVNDFTKEVITNSITQPTLHSDFAAQRV 180
|||||
Qy      181 YQIMEHDSYKRFKSETYLHLIEGRPQPTNLRSSRSFTYNDQDV 227
Db      181 YQIMEQDSYTRFLKSDIYLDMEGRPQPTNLRSSRSFTCNCFQDV 227
|||||
RESULT 5
US-09-206-639-4
; Sequence 4, Application US/09206639
; Patent No. US2002003477A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING
; NUMBER OF SEQUENCES: 5
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: US
;; ZIP: 94304
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/206,639
;; FILING DATE: 07-Dec-1998
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/748,483
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0157 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-855-0555
;; TELEFAX: 415-845-4166
;; TELEX: <Unknown>
;;
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 211 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GenBank
;; CLONE: 292037
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-206-639-4

Query Match 35.4%; Score 429.5; DB 9; Length 211;
Best Local Similarity 44.3%; Pred. No. 1.6e-33;
Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;

QY 4 SLVFFSQNMCSKSKTFFKLMHSGSKETSIEAKIR---AKEKRNRLSLLQLRPDPHGE 60
DB 3 SAMFLAVQHDRCRPMDKS-----AGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGK 57

QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDATFRFLKTEFSEENIEFWVACE 120
DB 58 PRTGKSKQQAIFKPSPEAQWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACE 117

QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQAOTLHSDFTAQSRV 180
DB 118 DFKTKSPQKLSSKARKIYTDIEKEAPKEINIDFQTKLIAQNIQEAATSGCFTTAQKRV 177

QY 181 YQLMEHDSYKRFLLKSETYLHLIEGRPORPT 210
DB 178 YSLMENNYPFLESEFYQDLCK-KPQITT 206

RESULT 6
US-10-258-371B-24
; Sequence 24, Application US/10258371B
; Publication No. US20040067903A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS-GAGNON, Alison
; APPLICANT: MURRAY, David L
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
; TITLE OF INVENTION: RGS18, AND USES THEREOF
; FILE REFERENCE: A3656 US PCT
; CURRENT APPLICATION NUMBER: US/10/258,371B
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: GB001883.334

Query Match 35.4%; Score 429.5; DB 9; Length 211;
Best Local Similarity 44.3%; Pred. No. 1.6e-33;
Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;

QY 4 SLVFFSQNMCSKSKTFFKLMHSGSKETSIEAKIR---AKEKRNRLSLLQLRPDPHGE 60
DB 3 SAMFLAVQHDRCRPMDKS-----AGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGK 57

QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDATFRFLKTEFSEENIEFWVACE 120
DB 58 PRTGKSKQQAIFKPSPEAQWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACE 117

QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQAOTLHSDFTAQSRV 180
DB 118 DFKTKSPQKLSSKARKIYTDIEKEAPKEINIDFQTKLIAQNIQEAATSGCFTTAQKRV 177

QY 181 YQLMEHDSYKRFLLKSETYLHLIEGRPORPT 210
DB 178 YSLMENNYPFLESEFYQDLCK-KPQITT 206

RESULT 7
US-10-408-765A-493
; Sequence 493, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 493
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-493

Query Match 35.4%; Score 429.5; DB 16; Length 211;
Best Local Similarity 44.3%; Pred. No. 1.6e-33;
Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;

QY 4 SLVFFSQNMCSKSKTFFKLMHSGSKETSIEAKIR---AKEKRNRLSLLQLRPDPHGE 60
DB 3 SAMFLAVQHDRCRPMDKS-----AGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGK 57

QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDATFRFLKTEFSEENIEFWVACE 120
DB 58 PRTGKSKQQAIFKPSPEAQWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACE 117

QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQAOTLHSDFTAQSRV 180
DB 118 DFKTKSPQKLSSKARKIYTDIEKEAPKEINIDFQTKLIAQNIQEAATSGCFTTAQKRV 177

;; PRIOR FILING DATE: 2000-08-02
;; PRIOR APPLICATION NUMBER: US60/200,786
;; PRIOR FILING DATE: 2000-04-28
;; NUMBER OF SEQ ID NOS: 38
;; SOFTWARE: Patent in version 3.2
;; SEQ ID NO 24
;; LENGTH: 211
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-258-371B-24

Query Match 35.4%; Score 429.5; DB 12; Length 211;
Best Local Similarity 44.3%; Pred. No. 1.6e-33;
Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;

QY 4 SLVFFSQNMCSKSKTFFKLMHSGSKETSIEAKIR---AKEKRNRLSLLQLRPDPHGE 60
DB 3 SAMFLAVQHDRCRPMDKS-----AGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGK 57

QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDATFRFLKTEFSEENIEFWVACE 120
DB 58 PRTGKSKQQAIFKPSPEAQWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACE 117

QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQAOTLHSDFTAQSRV 180
DB 118 DFKTKSPQKLSSKARKIYTDIEKEAPKEINIDFQTKLIAQNIQEAATSGCFTTAQKRV 177

QY 181 YQLMEHDSYKRFLLKSETYLHLIEGRPORPT 210
DB 178 YSLMENNYPFLESEFYQDLCK-KPQITT 206

RESULT 7
US-10-408-765A-493
; Sequence 493, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 493
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-493

Query Match 35.4%; Score 429.5; DB 16; Length 211;
Best Local Similarity 44.3%; Pred. No. 1.6e-33;
Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;

QY 4 SLVFFSQNMCSKSKTFFKLMHSGSKETSIEAKIR---AKEKRNRLSLLQLRPDPHGE 60
DB 3 SAMFLAVQHDRCRPMDKS-----AGSGHKSEKREKMKRTLLKDWKTRLSYFLQNSSTPGK 57

QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDATFRFLKTEFSEENIEFWVACE 120
DB 58 PRTGKSKQQAIFKPSPEAQWSEAFDELLASKYGLAAFRFLKSEFCEENIEFWLACE 117

QY 121 DFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTKEVIKSIQAOTLHSDFTAQSRV 180
DB 118 DFKTKSPQKLSSKARKIYTDIEKEAPKEINIDFQTKLIAQNIQEAATSGCFTTAQKRV 177

QY 181 YQMEHDSYKRLKSETYLHLIEGRPQPT 210
 Db 178 YSLMNNYSYRLESEFYQDLCK-KPQITT 206

RESULT 8

US-09-925-300-1507
 ; Sequence 1507, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 1507
 ; LENGTH: 220
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-300-1507

Query Match 35.4%; Score 429.5; DB 9; Length 220;
 Best Local Similarity 44.3%; Pred. No. 1.7e-33;
 Matches: 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;
 QY 4 SLVFFSQLNCFSEKFTFKLMHGSGKEETSIAKIR---AKEKENRLSLLQLRPDFHGE 60
 Db 12 SAMFLAVOCHDCRPMDKS-----AGSHKSEKREKXKRTLLKDWKTRLSYFLQNSSTPGK 66
 QY 61 TQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFPLKTEFSEENIERPWACE 120
 Db 67 PRIGKKSQQAQIKSPPEAQWSAFDELLASKTGLAAFRFLKSEFCENIEFWLACE 126
 QY 121 DFKCKKEPQIILKAKAIYEKFIQNDAPKEVNIIDFHTKEVIAKSTAQPTLHSFDTAQSRV 180
 Db 127 DFKTKSPQKLSKARKIVTDIEKEAPKEINIDFOTKTLIAQNIQENTSGCFTTAQKRV 186
 QY 181 YQMEHDSYKRLKSETYLHLIEGRPQPT 210
 Db 187 YSLMNNYSYRLESEFYQDLCK-KPQITT 215

RESULT 9

US-09-206-639-1
 ; Sequence 1, Application US/09206639
 ; Patent No. US20020034777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALING
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/206,639
 ; FILING DATE: 07-Dec-1998

CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/748,483
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0157 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0553
 ; TELEFAX: 415-845-4166
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 181 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Consensus
 ; CLONE: 57362
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-206-639-1

Query Match 35.2%; Score 427.5; DB 9; Length 181;
 Best Local Similarity 50.3%; Pred. No. 2e-33;
 Matches 84; Conservative 33; Mismatches 47; Indels 3; Gaps 1;
 QY 40 RAKEKENRLSLLQLRPDFHGE---TQASRSALLAKETRVSPPEAVKWAESFKLLSHRDG 96
 Db 15 RAKEIKLIGILLQKPDVSGDLVIPYNEKPEKPAKTQKTSLEALQWRDSDLKLLQNNYG 74
 QY 97 VDAFTFPLKTEFSEENIERPWACEDPKCKEPOQIILKAKAIYEKFIQNDAPKEVNIIDPH 156
 Db 75 LASFKSFLKSEFSEENLEFWDIEDYKTKSPAKWAEKAKQIYEFQTEAPKEVNIIDHF 134
 QY 157 TKRVIKASTAQPTLHSFDTAQSRVYQVMEDHSYKRLKSETYLHLIE 203
 Db 135 TKDITKXNLVPSLSLSDMAQRIHALMEKDSLPRFVRSEFYQELIK 181

RESULT 10
 US-10-258-371B-22
 ; Sequence 22, Application US/10258371B
 ; Publication No. US20040067903A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS-GAGNON, Alison
 ; APPLICANT: MURRAY, David L
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A NOVEL REGULATOR OF G PROTEIN SIGNALING,
 ; TITLE OF INVENTION: RGS18, AND USES THEREOF
 ; FILE REFERENCE: A3656 US PCT
 ; CURRENT APPLICATION NUMBER: US/10/258,371B
 ; CURRENT FILING DATE: 2003-06-04
 ; PRIOR APPLICATION NUMBER: GB001883.334-
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: US60/200,786
 ; PRIOR FILING DATE: 2000-04-28
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 22
 ; LENGTH: 181
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-258-371B-22

Query Match 35.2%; Score 427.5; DB 12; Length 181;
 Best Local Similarity 50.3%; Pred. No. 2e-33;
 Matches 84; Conservative 33; Mismatches 47; Indels 3; Gaps 1;
 QY 40 RAKEKENRLSLLQLRPDFHGE---TQASRSALLAKETRVSPPEAVKWAESFKLLSHRDG 96
 Db 15 RAKEIKLIGILLQKPDVSGDLVIPYNEKPEKPAKTQKTSLEALQWRDSDLKLLQNNYG 74

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2004, 16:14:26 ; Search time 25 Seconds.
(without alignments)
904,200 Million cell updates/sec

Title: US-09-894-749-4
Perfect score: 1214
Sequence: 1 MDMSLVFPSQLNMCSKEKT.....SRSTYNDQDVKSDVAIWL 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	429.5	35.4	211	2	I53020 G-O/G-1 switch reg
2	397.5	32.7	205	2	S78221 G-protein signalin
3	395.5	32.6	181	2	JC7228 G-protein signalin
4	393.5	31.5	519	2	S78089 G-protein signalin
5	345.5	28.5	196	2	S43436 B cell activation
6	293.5	24.2	251	2	S43576 C05B5.7 protein (c
7	293.5	24.2	254	2	G88571 protein C05B5.7 [i
8	291.5	24.0	181	2	T21035 hypothetical prote
9	291	24.0	169	2	T21034 hypothetical prote
10	290	23.9	244	2	T13580 hypothetical prote
11	277	22.8	173	2	S71812 RG810 protein - hu
12	275.5	22.7	533	2	T31002 hypothetical prote
13	242	19.9	544	2	JCS503 G-protein signalin
14	234	19.3	1387	2	JCS502 G-protein signalin
15	217	17.9	558	2	T21468 hypothetical prote
16	216.5	17.8	473	2	T19337 hypothetical prote
17	193	15.9	838	2	T08423 Axin homolog Axil
18	192.5	15.9	832	2	T08422 negative regulator
19	190.5	15.7	234	2	T28672 hypothetical prote
20	175	14.4	284	2	T15700 hypothetical prote
21	168.5	13.9	270	2	T22213 hypothetical prote
22	156	12.9	235	2	F89472 protein ZC53.7 [im
23	153	12.6	274	2	T22214 hypothetical prote
24	143	11.8	303	2	T29513 hypothetical prote
25	139.5	11.5	309	2	S61665 probable membrane
26	138	11.4	719	2	S60771 developmental regu
27	112.5	9.3	229	2	A89473 protein F52D2.2 [i
28	109.5	9.0	423	2	T15335 hypothetical prote
29	107.5	8.9	913	2	T31497 hypothetical prote

30	105.5	8.7	688	1	A39336 beta-adrenergic-re
31	104	8.6	1010	2	T41077 hypothetical struc
32	102	8.4	2748	2	S57976 nuclear migration
33	98.5	8.1	727	2	T26096 hypothetical prote
34	98	8.1	689	1	I56531 beta-adrenergic-re
35	98	8.1	2829	2	A42771 reticulocyte-bindi
36	97	8.0	688	1	JC1469 beta-adrenergic-re
37	96.5	7.9	901	2	S65161 hypothetical prote
38	93	7.7	704	2	S25371 beta-adrenergic-re
39	92	7.6	688	1	T17328 beta-adrenergic-re
40	92	7.6	792	2	T49989 hypothetical prote
41	92	7.6	1120	2	S67208 hypothetical prote
42	91.5	7.5	686	2	T15795 hypothetical prote
43	91.5	7.5	1031	1	A38713 kinesis heavy chai
44	91	7.5	449	2	G81419 hypothetical prote
45	91	7.5	851	2	S73939 oligopeptide trans

ALIGNMENTS

RESULT 1

I53020
G-O/G-1 switch regulatory protein 8 - human
N;Alternate names: helix-loop-helix phosphoprotein; regulator of G-protein signaling 2, ;
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I53020; I65984
R;Siderovski, D.P.; Heximer, S.P.; Forsdyke, D.R.
DNA Cell Biol. 13, 125-147, 1994
A;Title: A human gene encoding a putative basic helix-loop-helix phosphoprotein whose mR
A;Reference number: I53020; MUID:94235158; PMID:8179820
A;Accession: I53020
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-211 <RES>
A;Cross-references: GB:I13391; NID:G9292036; PIDN:AAA20680.1; PID:G9292037
A;Accession: I65984
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-211 <RE2>
A;Cross-references: GB:I13463; NID:G9292054; PIDN:AAC37587.1; PID:G9292055
C;Genetics:
A;Gene: GDB:RG82; G088
A;Map position: Iq31-1q31
A;Introns: 37/2; 71/2; 92/1; 147/3
C;Superfamily: B-cell activation protein BL34
C;Keywords: phosphoprotein

Query Match 35.4%; Score 429.5; DB 2; Length 211;
Best Local Similarity 44.3%; Pred. No. 4.6e-25;
Matches 93; Conservative 36; Mismatches 70; Indels 9; Gaps 3;

Qy	4	SLVFPFSQLNMCSKEKTFFKLMGSGKEETSIEAKIR--AKERNELSLLLORPDFHGE	60
Db	3	SAMFLAVHDCRPNMKG-----AGSGHKSEKREKMKRTLLKDWKTKLSYFLQNSSTPGK	57
Qy	61	TQASRSALLAKETRVSPPEEAQKWAESFDKLLSHRDGVDAFTRFIKTEFSEENIEFWVACE	120
Db	58	PTGKSKSQQAQAFIKFSPPEEAQLWSEAFDELLASKYGLAFAFLKSEFCENIEFWLACE	117
Qy	121	DFKCKEPPQIILKAKAIYEKFTQNDAPKEVNDFTHTKEVIKSIAPQTHSDTAQSRV	180
Db	118	DFKTKSPQKLSSKARKIYTDFTIEKAPKBNIDFQTKLIAQNIQEQATSCGCTTAQKRV	177
Qy	181	YQLMEHDSYKRFILKSETYLHLIEGRPQPT	210
Db	178	YSLMNNNSYRFLSESEFYQDLCK-KPQITT	206

RESULT 2

S78221

A;Cross-references: GB:S59049; NID:q299704; PIDN:AAB26289.1; PID:q299705

C;Genetics:

A;Gene: GDB:RGSI; IER1; IR20; IR20; BL34

A;Cross-references: GDB:439178; OMIM:600323

A;Map position: 1q31-1q31

C;Superfamily: B-cell activation protein BL34

C;Keywords: B-cell; phosphoprotein

Query Match 28.5%; Score 345.5; DB 2; Length 196;

Best Local Similarity 52.3%; Pred. No. 7.9e-19;

Matches 67; Conservative 24; Mismatches 36; Indels 1; Gaps 1;

QY 75 VSPERAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACEDFKCKEPOQIILK 134

DB 61 LSAEAWQWSQSLKLANQTCQNVFGSLKSEFSEENIEFWACEDYKK-TESDLLECK 119

QY 135 AKAIYEKFTQNDAPKEVNIIDFTKEVIKIAQIPLHSPDTAQSRVYQVMEHDSYKRLK 194

DB 120 ABEIYKAFVHSDAAQINIDFRTRESTAKKIKAPTTCFDEAKRVITYILMEXDSYPRFLK 179

QY 195 SETYLHLI 202

DB 180 SHIYLNLL 187

RESULT 6

S43576

C05B5.7 protein (clone C05B5) - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 13-Sep-1998

C;Accession: S43576

R;Northmore, B.

submitted to the EMBL Data Library, April 1994

A;Reference number: S43570

A;Accession: S43576

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <MOR>

A;Cross-references: EMBL:232679

C;Genetics:

A;Introns: 165/1; 197/3

C;Superfamily: B-cell activation protein BL34

Query Match 24.2%; Score 293.5; DB 2; Length 251;

Best Local Similarity 42.2%; Pred. No. 8e-15;

Matches 57; Conservative 30; Mismatches 37; Indels 11; Gaps 1;

QY 75 VSPERAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACEDPK 123

DB 16 VSPQRSVQPEALSYEMVYSWQSQFDTLMSFKGQKCFAEFLKSEYSDENILFWQACEELK 75

QY 124 KCKEPQOILKAKIYEKFTQNDAPKEVNIIDFTKEVIKIAQIPLHSPDTAQSRVYQV 183

DB 76 REKNSEKMEKARIYEDFISILSPKEVSLDSKVREIVNTNMGRPTQNTFEDAQHQIYQL 135

QY 184 MEHDSYKRLKSETY 198

DB 136 MARDSPRFLTSIFY 150

RESULT 7

G88571

protein C05B5.7 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001

C;Accession: G88571

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: G88571

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-254 <STO>

A;Cross-references: GB:chr_III; PIDN:CAA83595.1; PID:g3873995; GSPDB:GN00021; CESP:C05B5

A;Note: similar to Ir20 protein (human)

C;Genetics:

A;Gene: C05B5.7

A;Map position: 3

C;Superfamily: B-cell activation protein BL34

Query Match 24.2%; Score 293.5; DB 2; Length 254;

Best Local Similarity 42.2%; Pred. No. 8.1e-15;

Matches 57; Conservative 30; Mismatches 37; Indels 11; Gaps 1;

QY 75 VSPERAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACEDPK 123

DB 19 VSPQRSVQPEALSYEMVYSWQSQFDTLMSFKGQKCFAEFLKSEYSDENILFWQACEELK 78

QY 124 KCKEPQOILKAKIYEKFTQNDAPKEVNIIDFTKEVIKIAQIPLHSPDTAQSRVYQV 183

DB 79 REKNSEKMEKARIYEDFISILSPKEVSLDSKVREIVNTNMGRPTQNTFEDAQHQIYQL 138

QY 184 MEHDSYKRLKSETY 198

DB 139 MARDSPRFLTSIFY 153

RESULT 8

T21035

hypothetical protein F16H9.1b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000

C;Accession: T21035; T21272

R;Gardner, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19363

A;Accession: T21035

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-181 <W12>

A;Cross-references: EMBL:Z50005; PIDN:CAB54219.1; GSPDB:GN00028; CESP:F16H9.1b

A;Experimental source: clone F16H9

R;Gardner, A.

submitted to the EMBL Data Library, November 1995

A;Reference number: Z19398

A;Accession: T21272

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-181 <W12>

A;Cross-references: EMBL:Z67882; PIDN:CAB54230.1; GSPDB:GN00028; CESP:F16H9.1b

A;Experimental source: clone F22E10

C;Genetics:

A;Gene: CESP:F16H9.1b

A;Map position: X

A;Introns: 28/2; 43/2; 64/1; 103/3

C;Superfamily: B-cell activation protein BL34

Query Match 24.0%; Score 291.5; DB 2; Length 181;

Best Local Similarity 40.0%; Pred. No. 7.6e-15;

Matches 58; Conservative 31; Mismatches 51; Indels 5; Gaps 1;

QY 59 GETQASRSALLAKETRVSP-----EAVKWAESPDKLLSHRDGVDAFTFLKTEFSEENI 113

DB 23 GKPYVSGSVSVKKNQENDGPTTVEIVFGNSQSFENLMKHRAGQKYFAEFLKGYSDENI 82

QY 114 BFWACEDFKCKEPPQOILKAKIYEKFTQNDAPKEVNIIDFTKEVIKIAQIPLHSP 173

DB 83 LFWQACEELKREKVAEKIEEKARIYEDFISILSPKEVSLDSRVREIVNTNMGRPSASTF 142

QY 174 DTAQSRVYQVMEHDSYKRLKSETY 198

DB 143 DEANQIYTLMQRDSYPRFLASNLY 167

RESULT 9

RESOL1 9
 T21034
 hypothetical protein F16H9.1a - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T21034; T21270
 R:Gardner, A.
 submitted to the EMBL Data Library, July 1995
 A:Reference number: Z19363
 A:Accession: T21034
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-169 <W1>
 A:Cross-references: EMBL:Z50005; PIDN:CAA90295.1; GSPDB:GN00028; CESP:F16H9.1a
 A:Experimental source: clone F16H9
 R:Gardner, A.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19398
 A:Accession: T21270
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-169 <W12>
 A:Cross-references: EMBL:Z67882; PIDN:CAA91803.1; GSPDB:GN00028; CESP:F16H9.1a
 A:Experimental source: clone F22E10
 C:Genetics:
 A:Gene: CESP:F16H9.1a
 A:Map position: X
 A:Introns: 16/2; 31/2; 52/1; 91/3
 C:Superfamily: B-cell activation protein BL34

RESULT 10

```

RESULT 10
TI13580
hypothetical protein 52C10.2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: TI13580
R:Benos, P.
submitted to the EMBL Data Library, February 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17690
A:Accession: TI13580
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-244 <3EN>
A:Cross-references: EMBL:AL035311; PIDN:CAA22951.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0026309
A:Map position: X
A:Introns: 101/2; 127/2; 148/1
A>Note: EG:52C10.2
C:Superfamily: B-cell activation protein BL34

      Query Match      23.9%; Score 290; DB 2; Length 244;
      Best Local Similarity 46.5%; Pred. No. 1.4e-14;
      Matches 53; Conservative 23; Mismatches 38; Indels 0; Gaps 0;

QY 78 EFADVWASSFDKLASHRDGVDAFTFLKTFESENIEFWVACEDFKCKEPOQIILKKA 137
DB 131 EIRISWGSFQKLKSTAGRVQFONFLRSFSSSIEFLWACEDLKKNSPELVEEKAL 190

```

QY	138	IYEKFIQNDAPEKNIDFHTKEVIAKSIAQPTLHSFDTAQRVYQLMEHDSYKR	191
		: : : : : : : :	
Db	191	IVEDYSILSPREVSLDRVEEIVNRNWIETPTTFDEAOIQIYTLMRDSDSYR	244

RESULT 11

S71812
 RGS10 protein - human
 C; Species: Homo sapiens (man)
 C; Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999
 C; Accession: S71812
 R; Hunt, T.W.; Fields, T.A.; Casey, P.J.; Peralta, E.G.
 Nature 383, 175-177, 1996
 A; Title: RGS10 is a selective activator of Galpha(i) GTPase activity.
 A; Reference number: S71812; MUID:96371048; PMID:8774883
 A; Accession: S71812
 A; Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-173 <HUN>
 C; Superfamily: B-cell activation protein B134

RESULT 12

```

T31002
hypothetical protein F56B6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31002
R:Stellies, L.; Stellie, L.
submitted to the EMBL Data Library, September 1999
A:Description: The sequence of C. elegans cosmid F56B6.
A:Reference number: Z20957
A:Accession: T31002
A:Status: preliminary; translated from QB/EMBL/DD8U
A:Molecule type: DNA
A:Residues: 1-533 <STE>
A:Cross-references: EMBL:D64599; PIDN:AA04563.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Map position: X
A:Introns: 39/3; 235/2; 259/2; 322/3; 360/2; 405/1; 461/3; 503/2
A:Note: F56B6.2

Query Match      22.7%; Score 275.5; DB 2; Length 533;
Best Local Similarity 28.7%; Pred. No. 4.3e-13;
Matches          70; Conservative 44; Mismatches 79; Indels 51; Gaps 6;

QY      15  ESKEKTFKLMHGSGKEETSIAEKIAKEKNELSLLLQRPDPFHGTQASRS----- 66
Db      299  EINNEGFLLNKDQGRKQFPQKVARQ-----TFYEDPATGVSSAGSSVISNNTGG 351

QY      67  -----ALLAKETVSPEEAVKWAESDKLLSHRDGDVDAFT 101
Db      352  QVRIALKVIGPISRTLSTYLRSKMDLALSTSSLYPSRDDVQRQWSEISPELNNKPGCALFR 411

QY      102  RFLKTFESENTEFWVACEDFKKCKE-PQOILKAKAIYEKFTQNDAPKEWIDFTKEV 160

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 20, 2004, 12:32:00 ; Search time 14.5 Seconds
(without alignments)
843.896 Million cell updates/sec

Title: US-09-894-749-4

Perfect score: 12.4

Sequence: 1 MDMSLVFFSQLNMCSEKKT.....SRSTYTFDQVKSDVAIWL 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1214	100.0	235	1 RGS1_MOUSE	Q99pg4 mus musculus
2	1032	85.0	235	1 RGS1_HUMAN	Q9ns28 homo sapien
3	429.5	35.4	211	1 RGS2_HUMAN	P41220 homo sapien
4	428.5	35.3	211	1 RGS2_RAT	Q9kx30 rattus norv
5	427.5	35.2	181	1 RGS5_HUMAN	O15b39 homo sapien
6	426.5	35.1	211	1 RGS2_MOUSE	O08849 mus musculus
7	412.5	34.0	181	1 RGS5_RAT	P49800 rattus norv
8	407.5	33.6	180	1 RGS8_HUMAN	P57771 homo sapien
9	407.5	33.6	180	1 RGS8_RAT	P49804 rattus norv
10	406.5	33.5	181	1 RGS5_MOUSE	O08850 mus musculus
11	397.5	32.7	205	1 RGS4_HUMAN	P49798 homo sapien
12	397.5	32.7	205	1 RGS4_MOUSE	O08899 mus musculus
13	396	32.6	568	1 RGS3_MOUSE	Q9dc04 mus musculus
14	395.5	32.6	205	1 RGS4_RAT	P49799 rattus norv
15	383	31.5	519	1 RGS3_HUMAN	P49796 homo sapien
16	367.5	30.3	196	1 RGS1_MOUSE	Q9j125 mus musculus
17	363	29.9	202	1 RGS6_HUMAN	O15492 homo sapien
18	356.5	29.4	199	1 RGS6_RAT	P97428 rattus norv
19	356	29.3	201	1 RGS6_MOUSE	P97428 mus musculus
20	356	29.3	202	1 RGS6_BOVIN	O46471 bos taurus
21	347.5	28.6	196	1 RGS1_HUMAN	Q08116 homo sapien
22	311.5	25.7	216	1 RGSJ_RAT	O70521 rattus norv
23	309	25.5	374	1 RGSK_BOVIN	P79348 bos taurus
24	308	25.4	388	1 RGSJ_HUMAN	P76081 homo sapien
25	307	25.3	217	1 RGSJ_MOUSE	P49795 homo sapien
26	306.5	25.2	216	1 RGSJ_CHICK	Q9cx84 mus musculus
27	302	24.9	218	1 RGSJ_HUMAN	O9pwal gallus gall
28	300	24.7	159	1 RGS2_HUMAN	O14921 homo sapien
29	300	24.7	239	1 RGSJ_MOUSE	Q9qzb1 mus musculus
30	298	24.5	210	1 RGSJ_CHICK	O9pwa0 gallus gall
31	286	24.4	210	1 RGSJ_HUMAN	Q9hg66 homo sapien
32	285	24.3	210	1 RGSJ_MOUSE	Q9qzb0 mus musculus
33	293.5	24.2	201	1 RGS1_CABEL	P34280 caenorhabdi

ALIGNMENTS

RESULT 1

ID	RGS1_MOUSE	STANDARD;	PRT;	235 AA.
AC	Q99pg4;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Regulator of G-protein signaling 18 (RGS18).			
GN	RGS18.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BA;			
RX	PubMed=11042171;			
RA	Park I.K., Klug C.A., Li K., Jerabek L., Li L., Nanamori M.,			
RA	Neubig R.R., Hood L., Weissman I.L., Clarke M.F.;			
RT	"Molecular cloning and characterization of a novel regulator of			
RT	G-protein signaling from mouse hematopoietic stem cells.";			
RL	J. Biol. Chem. 276:915-923(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BDF1;			
RX	MEDLINE=21240406; PubMed=11342430;			
RA	Nagata Y., Oda M., Nakata H., Shozaki Y., Kozasa T., Todokoro K.;			
RT	"A novel regulator of G-protein signaling bearing GAP activity for			
RT	Galphai and Galphag in megakaryocytes.";			
RL	Blood 97:3051-3060(2001).			
CC	-!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE			
CC	ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO			
CC	THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(Q)-ALPHA.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- TISSUE SPECIFICITY: Expressed in bone marrow, spleen, fetal liver			
CC	and lung. At very low levels expressed in heart.			
CC	-!- SIMILARITY: Contains 1 RGS domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AF102685; AAG53657.1; -			
DR	EMBL; AB042807; BAB60723.1; -			
DR	HSSP; P49799; IAGR.			
DR	MGD; MG1:1927498; Rgs18.			
DR	GO; GO:0005737; C:cytoplasm; IDA.			
DR	GO; GO:0005096; F:GTPase activator activity; IDA.			
DR	GO; GO:0016299; F:Regulator of G-protein signaling activity; IDA.			
DR	GO; GO:0008277; P:regulation of G-protein coupled receptor pr. . . ; IDA.			
DR	InterPro; IPR000342; Regl_Gprotein.			
DR	Ffam; PF00615; RGS; 1.			

P49808 caenorhabdi
Q9cge5 mus musculu
O4365 homo sapien
Q92282 mus musculu
P49805 rattus norv
O54828 mus musculu
O46469 bos taurus
O75916 homo sapien
P49802 homo sapien
P57492 mus musculu
O08773 rattus norv
P49758 homo sapien

34 291 24.0 169 1 RGS2_CABEL
35 286.5 23.6 181 1 RGS1_MOUSE
36 277 22.8 173 1 RGS1_HUMAN
37 259.5 21.4 409 1 RGS6_MOUSE
38 248 20.4 677 1 RGS9_RAT
39 247 20.3 675 1 RGS9_MOUSE
40 246 20.3 484 1 RGS9_BOVIN
41 246 20.3 674 1 RGS9_HUMAN
42 245.5 20.2 495 1 RGS7_HUMAN
43 243 20.0 547 1 RGS6_MOUSE
44 242 19.9 544 1 RGS6_RAT
45 241.5 19.9 567 1 RGS6_HUMAN

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DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gprotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS00132; RGS; 1.
KW Signal transduction inhibitor.
FT DOMAIN 86 202
SQ SEQUENCE 235 AA; 27610 MW; 6433435AC1CBQF08 CRC64;

Query Match 100.0%; Score 1214; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-84; Mismatches 0; Indels 0; Gaps 0;
Matches 235; Conservative 0;

QY 1 MDMSLVFFSQNLNCCSKETFFKLMHSGSKETSIEAKIRAKENRNLISLLIQRPDPHGE 60
DB 1 MDMSLVFFSQNLNCCSKETFFKLMHSGSKETSIEAKIRAKENRNLISLLIQRPDPHGE 60
QY 61 TQASRSALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACE 120
DB 61 TQASRSALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACE 120
QY 121 DFKKCKEPOQIILKAKAIYEKTIQNDAPKEVNI DFTKEVIKSAIQPTLHSDVAVLW 180
DB 121 DFKKCKEPOQIILKAKAIYEKTIQNDAPKEVNI DFTKEVIKSAIQPTLHSDVAVLW 180
QY 181 YQIMEHDSYKRFKSKSTYHLIEGRPQPTNLRSSRSPTYNDFQVKSQDVAVLW 235
DB 181 YQIMEHDSYKRFKSKSTYHLIEGRPQPTNLRSSRSPTYNDFQVKSQDVAVLW 235

RESULT 2
RGS1_HUMAN STANDARD; PRT; 235 AA.
AC Q9NS28;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Regulator of G-protein signaling 18 (RGS18).
GN RGS18 OR RGS13.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Yuan Z., He L., Cao X.;
RT "A novel regulator of G-protein signaling.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Cagnon A.W., Murray D.L., Leadley R.J. Jr.;
RT "Cloning and characterization of a novel regulator of G-protein signaling in human platelets.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX PubMed=11042171;
RA Park I.K., Klug C.A., Li K., Jerabek L., Li L., Nanamori M.,
RA Neubig R.R., Hood L., Weissman I.L., Clarke M.F.;
RT "Molecular cloning and characterization of a novel regulator of G-protein signaling from mouse hematopoietic stem cells.";
RL J. Biol. Chem. 276:915-923(2001).
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,

```

```

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE ACTIVITY OF G PROTEIN ALPHA SUBUNIT THEREBY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(1)-ALPHA AND G(Q)-ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in peripheral leukocytes, bone marrow, spleen and fetal liver.
CC -!- SIMILARITY: Contains 1 RGS domain.
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CC
DR EMBL; AF076642; AAF80227.1; -
DR EMBL; AF268036; AAK58589.1; -
DR EMBL; BC020632; AAH20632.1; -
DR HSSP; P49799; IAGR.
DR Genew; HGNC:14261; RGS18.
DR MIM; 607192; -
DR InterPro; IPR000342; Regl_Gprotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gprotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS00132; RGS; 1.
KW Signal transduction inhibitor.
FT DOMAIN 86 202
FT CONFLICT 226 227 DV -> ML (IN REF. 3).
SQ SEQUENCE 235 AA; 27582 MW; 973ABDE8EC7DE3D5 CRC64;

Query Match 85.0%; Score 1032; DB 1; Length 235;
Best Local Similarity 83.8%; Pred. No. 8.2e-71;
Matches 197; Conservative 19; Mismatches 19; Indels 0; Gaps 0;

QY 1 MDMSLVFFSQNLNCCSKETFFKLMHSGSKETSIEAKIRAKENRNLISLLIQRPDPHGE 60
DB 1 METTLFFSQNLNCCSKETFFKLMHSGSKETSIEAKIRAKENRNLISLLIQRPDPHGE 60
QY 61 TQASRSALLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACE 120
DB 61 TRSSRSGLAKETRVSPEEAVKWAESFDKLLSHRDGVDAFTFLKTEFSEENIEFWACE 120
QY 121 DFKKCKEPOQIILKAKAIYEKTIQNDAPKEVNI DFTKEVIKSAIQPTLHSDVAVLW 180
DB 121 DFKKCKEPOQIILKAKAIYEKTIQNDAPKEVNI DFTKEVIKSAIQPTLHSDVAVLW 180
QY 181 YQIMEHDSYKRFKSKSTYHLIEGRPQPTNLRSSRSPTYNDFQVKSQDVAVLW 235
DB 181 YQIMEHDSYKRFKSKSTYHLIEGRPQPTNLRSSRSPTYNDFQVKSQDVAVLW 235

RESULT 3
RGS2_HUMAN STANDARD; PRT; 211 AA.
ID RGS2_HUMAN
AC P41220;
DT 01-FEB-1995 (Rel. 31, Created)

```

DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Regulator of G-protein signaling 2 (RGS2) (GO/GI switch regulatory
DE protein 8).
GN RGS2 OR GOS8.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=placenta;
RX MEDLINE=942325158; PubMed=8179820;
RA Siderovski D.P., Heximer S.P., Forsdyke D.R.;
RT "A human gene encoding a putative basic helix-loop-helix
RT phosphoprotein whose mRNA increases rapidly in cycloheximide-treated
RT blood mononuclear cells.";
RL DNA Cell Biol. 13:125-147(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Fuhr H.L. III, Ikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Bagguley C.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=urinary bladder;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=95371353; PubMed=7643615;
RA Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W.,
RA Minden M.D., Siderovski D.P.;
RT "Differential expression of a basic helix-loop-helix phosphoprotein
RT gene, GOS8, in acute leukemia and localization to human chromosome
RT 1q31.";
RL Leukemia 9:1291-1298(1995).
RN [6]
RP PHOSPHORYLATION.
RX MEDLINE=21101914; PubMed=11063746;
RA Cunningham M.L., Waldo G.L., Hollinger S., Hepler J.R., Harden T.K.;
RT "Protein kinase C phosphorylates RGS2 and modulates its capacity for
RT negative regulation of Galphai1 signaling.";
RL J. Biol. Chem. 276:5438-5444(2001).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACUTE MYELOGENOUS LEUKEMIA (AML)
CC AND IN ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).

CC -!- PTM: Phosphorylated by protein kinase C.
CC -!- SIMILARITY: Contains 1 RGS domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L13391; AAC20680.1; -;
DR EMBL; L13463; AAC37587.1; -;
DR EMBL; AF439326; AAM12640.1; -;
DR EMBL; AL035407; CAB62512.1; -;
DR EMBL; BC007049; AAH07049.1; -;
DR PIR; I53020; I53020.
DR HSSP; P49799; IAGR.
DR Genew; HGNC:9998; RGS2.
DR MIM; 600861; -;
DR GO; GO:0005516; F:calmodulin binding; TAS.
DR GO; GO:0005096; F:GTPase activator activity; TAS.
DR GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; TAS.
DR InterPro; IPR000342; Regl_Gprotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gprotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
KW Signal transduction inhibitor; Cell cycle; Phosphorylation.
FT DOMAIN 83 199 RGS.
SQ SEQUENCE 211 AA; 24382 MW; EFFE4AE47EF9AD8F CRC64;
Query Match 35.48; Score 429.5; DB 1; Length 211;
Best Local Similarity 44.3%; Pred. No. 1.4e-25;
Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;
QY 4 SLVFFSGLNLCESKEKTFKLMHGSGKEETSIEAKIR---AKKRNRLSLLLQRPDPHGE 60
DB 3 SAMPFLAVQHDRCRPMDKS-----AGSGHKSEKREKMKRTLKDKWKTLSYFLQNSSTPGK 57
QY 61 TQASRSALLAKETRVSPPEEAVKVAESPDKLLSHRDGDVATRLFKTEFSEENIEFWFACE 120
DB 58 PTKGSKQQAFAFKPSPEEAQLWSEAFDELLASKYGLAFAFLKSFCEENIEFWFACE 117
QY 121 DFKKCKEPQOILKAKAIVKFKTQNDAPKEVNDFTHTKEVIAKSAOPTLHSDTAQSRV 180
DB 118 DFKATKSPQLSSKARKIYDFDIKEAPKEINIDFQTKTLIAQNIQEAATSGCFTTAQXRV 177
QY 181 YQLMEHDSYKRFKSELYHLIEGRPQPT 210
DB 178 YSLMENNYPFLSEFYLCK-KPQITT 206
RESULT 4
RGS2 RAT ID RGS2 RAT STANDARD; PRT; 211 AA.
AC Q9UHX0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Regulator of G-protein signaling 2 (RGS2).
GN RGS2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Thoracic aorta;
RX MEDLINE=20159060; PubMed=10692485;
RA Grant S.L., Lassegue B., Griendling K.K., Ushio-Fukai M., Lyons P.R.,
RA Alexander R.W.;

```

RT "Specific regulation of RGS2 messenger RNA by angiotensin II in
RT cultured vascular smooth muscle cells.";
RL Mol. Pharmacol. 57:460-467(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar; TISSUE=Brain;
RA Taymans J.-M., Wintemolders C., Te Riele P., Jurzak M.,
RA Groenewegen H.J., Leysen J.E., Langlois X.;
RT "A detailed distribution study of RGS2 messenger RNA and protein in
RT the rat brain.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ko J.K., Kim I.S., Park D.H.;
RT "PTH induced RGS cDNA sequence in rat osteoblast-like UMR106 cell.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-100 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=21302414; PubMed=11409749;
RA Robinson E.A., Wurch T., Pauwels P.J.;
RT "Haloperidol and clozapine differently affect RGS2 mRNA expression in
RT rat brain.";
RL NeuroReport 12:1731-1735(2001).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G-PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS
CC (BY SIMILARITY).
CC -!- PTM: Phosphorylated by protein kinase C (By similarity).
CC -!- SIMILARITY: Contains 1 RGS domain.
CC -----
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CC or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL; AF279918; AAF85981.1; -
DR EMBL; AF218337; AAK03375.1; -
DR EMBL; AY043246; AAK85309.1; -
DR EMBL; AJ318489; CAC44900.1; -
DR HSSP; P49799; IAGR.
DR InterPro; IPR000342; Regl_Gproteins.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50132; RGS; 1.
KW Signal transduction inhibitor; Cell cycle; Phosphorylation.
FT DOMAIN 83 199
FT SEQUENCE 211 AA; 24323 MW; 84B5525CB41EA964 CRC64;
Query Match 35.3%; Score 428.5; DB 1; Length 211;
Best Local Similarity 44.3%; Pred. No. 1.7e-25;
Matches 93; Conservative 39; Mismatches 69; Indels 9; Gaps 3;
QY 4 SLVFFSOLNWCSSKEKTPFKLMHSGSKETSIEAKIR---AKEKNRLSLILQRPDPHGE 60
Db 3 SAMFLAVQHCDCVPMDS-----AGNPKVKEKRNKRTLLDKWKTLSYFLQNSSTPGK 57
QY 61 TQASRALLAKTRVSPERAVKWSFDKLLSHRGVDVAFTRFLKTERSEENIEFWACE 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 58 PTKGKSKQQTTPKPSPEALLWAFDELLASKYGLAFAFLKSEFCEENIEFWACE 117
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DFKCKEPPQIILKAKIYEKIQNDAPKEVNIDFHTKEVIAKSTAOPTLHSDFAQSRV 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 DFKKTSKPKLSKAKIYTDIEKAPKEINIDFQTKLIAQNIQEAISGCTTAAQKV 177
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 YQMEHDSYKFLKSTYHLIEGRPQRT 210
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 YSLMNNYSYRFESEFYQDLCK-KPQITT 206
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 5
 RGS5 HUMAN
 ID RGS5_HUMAN STANDARD; PRT; 181 AA.
 AC O15539.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Regulator of G-protein signaling 5 (RGS5).
 GN RGS5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chatterjee T.K., Fisher R.A.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Neuroblastoma;
 RC MEDLINE=98419174; PubMed=9747037;
 RA Seki N., Sugano S., Suzuki Y.-I., Nakagawara A., Ohira M.,
 RA Muramatsu M.-A., Saito T., Hori T.;
 RT "Isolation, tissue expression, and chromosomal assignment of human
 RT RGS5, a novel G-protein signaling regulator gene.";
 RL J. Hum. Genet. 43:202-205(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=99403338; PubMed=10471929;
 RA Cismowski M.J., Takesono A., Ma C., Lizano J.S., Xie X.,
 RA Fuernkranz H., Lanier S.M., Duzic E.;
 RT "Genetic screens in yeast to identify mammalian nonreceptor modulators
 RT of G-protein signaling.";
 RL Nat. Biotechnol. 17:878-883(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.C.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G-PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(O)-ALPHA,
 CC BUT NOT TO G(S)-ALPHA (BY SIMILARITY).
 CC -!- SIMILARITY: Contains 1 RGS domain.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
 CC EMBL; AF030108; AAB84001.1; -;
 CC EMBL; AB008109; BAA22889.1; -;
 CC EMBL; AF159570; AAD40957.1; -;
 CC EMBL; AF493929; AAM12643.1; -;
 CC EMBL; BC030059; AAH30059.1; -;
 CC HSP; P49799; IAGR.
 CC Genew; HGNC:10001; RGS5.
 CC MIM; 603276; -.

CC GO; GO:0005096; F:GTPase activator activity; TAS.
 CC GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; TAS.
 CC InterPro; IPR000342; Regl_Gprotein.

CC Pfam; PF00615; RGS; 1.
 CC PRINTS; PR01301; RGSPTOPEIN
 CC ProDom; PD001580; Regl_Gprotein; 1.
 CC SMART; SM00315; RGS; 1.
 CC PROSITE; PS50132; RGS; 1.
 CC Signal transduction inhibitor.
 CC FT DOMAIN 64 180 RGS.
 CC SEQUENCE 181 AA; 20946 MW; 2E08CB0175DE7687 CRC64;

Query Match 35.2%; Score 427.5; DB 1; Length 181;
 Best Local Similarity 50.3%; Pred. No. 1.7e-25;
 Matches 84; Conservative 33; Mismatches 47; Indels 3; Gaps 1;

QY 40 RAKEKRNLSLLQRPDPHGE--TQASRALLAKETRVSPPEAVKWAESFDKLLSHRDG 96
 DB 15 RAKEIKILGILLQRPDSVGLDIVYNEKPEKPAKTQKTSLEALQWRDSDLKLLQNYG 74
 QY 97 VDAFTFRFKTEPSENIWFVACEDFKCKEQQIILKAKAIYEKFIQNDAPKEVNIIDFH 156
 DB 75 LASFKSFLKSEFSENIWFVACEDFKCKEQQIILKAKAIYEKFIQNDAPKEVNIIDFH 134
 QY 157 TKEVIAKSIQAOTLHSDFTAQSRVQLMEHDSYKFLAKSETVHLIE 203
 DB 135 TQDIWKLVESLSFDMQAQRHAKMEKSLPRFVSEFYQELIK 181

RESULT 6
 RGS2_MOUSE
 ID RGS2_MOUSE STANDARD; PRT; 211 AA.
 AC O08349; Q91WX1; Q9JL24;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Regulator of G-protein signaling 2 (RGS2).
 GN RGS2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1] _TaxID:10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97236828; PubMed=9079700;
 RA Chen C., Zheng B., Han J., Lin S.C.;
 RT "Characterization of a novel mammalian RGS protein that binds to
 RT Galpha proteins and inhibits pheromone signaling in yeast.";
 RL J. Biol. Chem. 272:8679-8685 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=20243874; PubMed=10779778;
 RA Reif K., Cyster J.G.;
 RT "RGS molecule expression in lymphoid B lymphocytes and ability to
 RT down-regulate chemotaxis to murine chemokines.";
 RL J. Immunol. 164:4720-4729 (2000).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Shen Q.-X., Wang J., Huang Z.-P.;
 RT "Identification of novel endometrial and embryonic factors involved in
 RT mouse embryo implantation.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS.
 CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
 CC -!- PTM: Phosphorylated by protein kinase C (By similarity).
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC -----
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CC EMBL; U67187; AAB50617.1; -;
 CC EMBL; AF215668; AAF34625.1; -;
 CC EMBL; AF432916; AAL28114.1; -;
 CC HSP; P49799; IAGR.
 CC MGD; MGI:1098271; RGS2.
 CC InterPro; IPR000342; Regl_Gprotein.
 CC Pfam; PF00615; RGS; 1.
 CC PRINTS; PR01301; RGSPTOPEIN.
 CC ProDom; PD001580; Regl_Gprotein; 1.
 CC SMART; SM00315; RGS; 1.
 CC PROSITE; PS50132; RGS; 1.
 CC Signal transduction inhibitor; Cell cycle; Phosphorylation.
 CC FT DOMAIN 83 199 RGS.
 CC CONFLICT 39 40 KD -> NH (IN REF. 1).
 CC CONFLICT 78 79 QL -> HV (IN REF. 1).
 CC CONFLICT 78 79 QL -> DV (IN REF. 3).
 CC SEQUENCE 211 AA; 24294 MW; 5D6E25C2BC7E7FA CRC64;

Query Match 35.1%; Score 426.5; DB 1; Length 211;
 Best Local Similarity 44.3%; Pred. No. 2.4e-25;
 Matches 93; Conservative 38; Mismatches 70; Indels 9; Gaps 3;

QY 4 SLVFFSQLNMCSEKKEKTFPKLMHSGSKEETSIPAKIR--AKKRNRLSLLQRPDPHGE 60
 DB 3 SAMFLAVCHDQVPMKXS-----AGNGPKVKEKREKVKRLLKDKWTRLSYFLQNSAPGX 57
 QY 61 TQASRALLAKETRVSPPEAVKWAESFDKLLSHRDGVDATRLKTEPSENIWFVACE 120
 DB 58 PKTGKKSQQTFTKPSPEEAQLWAEAPDELLASKYGLAFAFLKSEFCSENIWFVACE 117
 QY 121 DFKKCKEPPQIILKAKAIYEKFIQNDAPKEVNIIDFTKVIKASIAQPTLHSDFTAQSRV 180
 DB 118 DFKKCKEPPQIILKAKAIYEKFIQNDAPKEVNIIDFTKVIKASIAQPTLHSDFTAQSRV 177
 QY 181 YQLMEHDSYKFLKSETVHLIEGRQRPRT 210
 DB 178 YSLMENNYSRPFLESEFYQDLCK-KPQITT 206

RESULT 7
 RGS5_RAT
 ID RGS5_RAT STANDARD; PRT; 181 AA.
 AC P49800; Q9JKD7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Regulator of G-protein signaling 5 (RGS5).
 GN RGS5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kirsch T., Lipoldt A., Wellner M., Haller H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 95-161 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96140645; PubMed=8548815;
RA Koelle M.R., Horvitz H.R.;
RT "EGL-10 regulates G protein signaling in the C. elegans nervous
system and shares a conserved domain with many mammalian proteins.";
RL Cell 84:115-125 (1996).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
ACTIVITY OF G PROTEIN ALPHA SUBUNIT THEREBY DRIVING THEM INTO
THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(O)-ALPHA,
BUT NOT TO G(S)-ALPHA (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 RGS domain.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; AF241259; AAF73424.1; -;
DR EMBL; U32435; AAC52372.1; -;
DR HSSP; P49799; IAGR.
DR InterPro; IPR000342; Regl_Gproteins.
DR PRINTS; PR01301; RGS-1.
DR PRODOM; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
KW Signal transduction inhibitor.
FT DOMAIN 64 180
FT SEQUENCE 181 AA; 21052 MW; 9C179CE08B82C03 CRC64;
QY Query Match 34.0%; Score 412.5; DB 1; Length 181;
Best Local Similarity 49.1%; Pred. NO. 2.2e-24;
Matches 86; Conservative 27; Mismatches 41; Indels 21; Gaps 2;
QY 40 RAKEENRLLSLQRPDPFHGETQASRSAL-----LAKETRVSPPEAVKWAESF 87
Db 15 RAKEIKIKLILQKPD-----SAVDLIPYNEKPEKPAKHKPSLEEVLOWRQL 65
QY 88 DKLLSHRDGVDATRELFKTEFSEENIEFWACEDFKCKEPOQIILKAKAIYEKFIQND 147
Db 66 DKLLQSNYGFASPKFLKSEFSEENLEFWACENYKIKSPIKMAEKAQIYEETQTEA 125
QY 148 PKEVNIDFTKTEFSEENIEFWACEDFKCKEPOQIILKAKAIYEKFIQND 202
Db 126 PKEVNIDFTKTEFSEENIEFWACEDFKCKEPOQIILKAKAIYEKFIQND 180
RESULT 8
RGS8_HUMAN STANDARD; PRT; 180 AA.
ID RGS8_HUMAN
AC P5771;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Regulator of G-protein signaling 8 (RGS8).
GN RGS8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2118927; PubMed=11318611;

RA Sood R., Bonner T.I., Malakowska I., Stephan D.A., Robbins C.M.,
RA Connors T.D., Morgenbesser S.D., Su K., Faruque M.U., Pinkett H.,
RA Graham C., Baxevas A.D., Klinger K.W., Landes G.M., Trent J.M.,
RA Carpten J.D.;
RT "Cloning and characterization of 13 novel transcripts and the human
RGS8 gene from the 1q25 region encompassing the hereditary prostate
cancer (HPC1) locus";
RL Genomics 73:211-222 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
ACTIVITY OF G PROTEIN ALPHA SUBUNIT THEREBY DRIVING THEM INTO
THEIR INACTIVE GDP-BOUND FORM. PREFERENTIALLY BINDS TO G(O)-ALPHA
AND G(I)-ALPHA-3 (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 RGS domain.
CC
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CC
CC EMBL; AF297015; AAG45337.1; -;
DR EMBL; AF300649; AAG18443.1; -;
DR HSSP; P49799; IAGR.
DR Genew; HGNC.16810; RGS8.
DR MIM; 607189;
DR InterPro; IPR000342; Regl_Gproteins.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-1.
DR PRODOM; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS0132; RGS; 1.
KW Signal transduction inhibitor.
FT DOMAIN 56 171
FT CONFLICT 1 9
FT DONAIN 1 9
FT SEQUENCE 180 AA; 20917 MW; 198965B4C27F64C9 CRC64;
QY Query Match 33.6%; Score 407.5; DB 1; Length 180;
Best Local Similarity 47.7%; Pred. NO. 5.2e-24;
Matches 83; Conservative 32; Mismatches 50; Indels 9; Gaps 2;
QY 40 RAKEENRLLSLQRPDPFHGETQASRSALLAKE-----TRVSPPEAVKWAESFKLLSHR 94
Db 9 RNMGRTRLCGLSHKSD-----SCSDFTAILPDNRLKRLSTEEATRWADSDVLLSHK 64
QY 95 DGYDAFTRFKTEFSEENIEFWACEDFKCKEPOQIILKAKAIYEKFIQNDAPKEVND 154
Db 65 YGVAFAFTRFKTEFSEENIEFWACEDFKCKEPOQIILKAKAIYEKFIQNDAPKEVND 124
QY 155 FHTKEVIKSIQPTLHSDFTAQSRVYQLMEHDSYKRFKSETYLHIEGRPOR 208
Db 125 FQTEATKRLQPSLTCPDQAQGVHSLMEKDSYKRFKSETYLHIEGRPOR 178
RESULT 9
RGS8_RAT STANDARD; PRT; 180 AA.
ID RGS8_RAT
AC P49804;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Regulator of G-protein signaling 8 (RGS8).
GN RGS8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN
 RN SEQUENCE FROM N.A., AND FUNCTION.
 RC TISSUE=Hippocampus;
 RA MEDLINE=98054153; PubMed=9394004;
 RA Saitoh O., Kubo Y., Miyatani Y., Asano T., Nakata H.;
 RT "RG88 accelerates G-protein-mediated modulation of K⁺ currents.";
 RL Nature 390:525-528 (1997).
 RN
 RN SEQUENCE OF 87-153 FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=96140645; PubMed=8548815;
 RA Koelle M.R., Horvitz H.R.;
 RT system and shares a conserved domain with many mammalian proteins.";
 RL Cell 84:115-125 (1996).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. PREFERENTIALLY BINDS TO G(O)-ALPHA
 CC AND G(I)-ALPHA-3
 CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN. VERY
 CC LITTLE EXPRESSION DETECTED IN OTHER TISSUES.
 CC -!- DEVELOPMENTAL STAGE: DETECTED IN 13-DAY OLD EMBRYOS. EXPRESSION
 CC INCREASES GRADUALLY IN LATER EMBRYOS AND MARKEDLY IN NEONATES TO
 CC ADULTS.
 CC -!- SIMILARITY: Contains 1 RGS domain.
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 CC
 DR EMBL; AB006013; BAA23680.1; -;
 DR EMBL; U32432; AAC52369.1; -;
 DR HSP; P49799; IAGR.
 DR InterPro: IPR000342; RegI_Gprotein.
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 DR ProDom; PD001580; RegI_Gprotein; 1.
 DR SMART; SM00315; RGS; 1.
 DR PROSITE; PS00132; RGS; 1.
 DR SIGNAL; PS00132; RGS; 1.
 KW Signal transduction inhibitor.
 FT DOMAIN 56 171
 SQ SEQUENCE 180 AA; 20949 MW; 00FC35B4C278B557 CRC64;
 Query Match 33.6%; Score 407.5; DB 1; Length 180;
 Best Local Similarity 47.7%; Pred. No. 5.2e-24;
 Matches 83; Conservative 32; Mismatches 50; Indels 9; Gaps 2;
 QY 40 RAKEKNRLSLQLLPDPHGETQASRSALLAXE-----TRVSPPEAVKWAESFDKLLSHR 94
 Db 9 RNKGNRLTGLSHKSD-----SCSFTALPKPKRALKRLSTKTEATKWAISFDVLLSHK 64
 QY 95 DGVDAFTRELFKTEFSEENIEFWACEDFKCKEPOQILKAKAIYEKFIQNDAPKEVND 154
 Db 65 YGVAAPRAFLKTEFSEENIEFWACEDFKCKEPOQILKAKAIYEKFIQNDAPKEVND 124
 QY 155 FTKKEVIAKSIQPLHSDTQASRYQIMEDSKYKRLKSTYLHLLEGPRQ 208
 Db 125 FQTREATRNQMEPSLTCPDQAGKVHLMKXDSYPRFLRSKMYLDLLSQSORR 178
 RESULT 10
 RGSS MOUSE
 ID RGSS MOUSE STANDARD; PRT; 181 AA.
 AC O08850; Q9D0Z2;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Regulator of G-protein signaling 5 (RGSS).
 GN MGS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97236828; PubMed=9079700;
 RA Chen C., Zheng B., Han J., Lin S.C.;
 RT "Characterization of a novel mammalian RGS protein that binds to
 RL Galpha proteins and inhibits pheromone signaling in yeast.";
 J. Biol. Chem. 272:8679-8685 (1997).
 RN
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gusticich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momodets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seitz T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weita C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN
 RN SEQUENCE FROM N.A.
 RP STRAIN=FVB/N; TISSUE=Mammary gland;
 RC MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield F.S., Krzywinski M.I., Skalska U., Smalus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS. THEREBY DRIVING THEM INTO
 CC THEIR INACTIVE GDP-BOUND FORM. BINDS TO G(I)-ALPHA AND G(O)-ALPHA,
 CC BUT NOT TO G(S)-ALPHA.
 CC -!- TISSUE SPECIFICITY: Expressed in heart and muscle.
 CC -!- SIMILARITY: Contains 1 RGS domain.
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CC  DR EMBL; U67188; AAB50618.1; -.
CC  DR EMBL; AX004165; BAB23201.1; -.
CC  DR EMBL; BC037683; AAH37683.1; -.
CC  DR HSSP; P49799; IAGR.
CC  DR MGD; MGI:1098434; Rgs8.
CC  DR InterPro; IPR000342; Regl_Gproteins.
CC  DR Pfam; PF00615; RGS; 1.
CC  DR PRINTS; PR01301; RGSPTROTIN.
CC  DR ProDom; PD001580; Regl_Gproteins; 1.
CC  DR SMART; SM00315; RGS; 1.
CC  DR PROSITE; PS0132; RGS; 1.
CC  DR Signal transduction inhibitor.
CC  DR DOMAIN 64 180 RGS.
CC  DR CONFLICT 49 50 KA -> NG (IN REF. 1).
CC  DR CONFLICT 77 77 S -> T (IN REF. 1).
CC  DR SEQUENCE 181 AA; 21085 MW; B4B561CFE3DA9630 CRC64;
CC  Query Match 33.5%; Score 406.5; DB 1; Length 181;
CC  Best Local Similarity 48.3%; Pred. NO. 6.3e-24;
CC  Matches 85; Conservative 29; Mismatches 41; Indels 21; Gaps 2;
CC
CC  QY 40 RAKEKENRLLLQRPDHFGEHCASRL-----LAKETRVSPPEAKVWASSF 97
CC  DB 15 RAKEIKIKILLQKPD-----SAVDLVPNEKEPKAKAHKSLEVLQWRSL 65
CC  QY 88 DKLLSHRDGVDAFTFLKTFESENIEFWACEDFKCKEPOQIILKAIYEKFIQND 147
CC  DB 66 DKLLQNSYGFAGFKSLKSEFSEENLEFWACENYKIKSPIKVAKAKQIYEKFIQEA 125
CC  QY 148 PKEVNIIDFTKVEIAKSIQAOTLHSPDFAQSRVQYLMEDSDVKRFLKSETYLHLIE 203
CC  DB 126 PKEVNIIDFTKTOIKTNLVEPSRFDLQAKRIYALMEKDSLPFRVSRSEFYKELIK 181
CC
CC  RESULT 11
CC  RGS4_HUMAN STANDARD; PRT; 205 AA.
CC  AC P49798;
CC  DT 01-OCT-1996 (Rel. 34, Created)
CC  DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC  DE 15-MAR-2004 (Rel. 43, Last annotation update)
CC  DE Regulator of G-protein signaling 4 (RGS4) (RGP4).
CC  GN RGS4.
CC  OS Homo sapiens (Human).
CC  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC  OX NCBI_TaxID=9606;
CC  [1]
CC  SEQUENCE FROM N.A.
CC  RX MEDLINE=96178495; PubMed=8602223;
CC  RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
CC  RT "Inhibition of G-protein-mediated MAP kinase activation by a new
CC  RT mammalian gene family."
CC  RL Nature 379:742-746 (1996).
CC  RN [2]
CC  SEQUENCE FROM N.A.
CC  RC TISSUE=Brain, and Uterus;
CC  RA Pahl H.L. III, Ikeda S.R., Aronstam R.S.;
CC  RT "cDNA clones of human proteins involved in signal transduction
CC  RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
CC  RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
CC  RN [3]
CC  SEQUENCE FROM N.A.
CC  RC TISSUE=Brain;
CC  RX MEDLINE=22388257; PubMed=12477932;
CC  RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC  RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC  RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC  RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
CC  RA Diatchenko L., Matusina K., Farmer A.A., Rubin A.A., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA [4]
RA PALMITOYLATION.
RA MEDLINE=20076507; PubMed=10608901;
RA Tu Y., Popov S., Slaughter C., Ross E.M.;
RA "Palmitoylation of a conserved cysteine in the regulator of G protein
RA signaling (RGS) domain modulates the GTPase-activating activity of
RA RGS4 and RGS10.";
RA J. Biol. Chem. 274:38260-38267(1999).
RA [5]
RA INHIBITION.
RA MEDLINE=98421527; PubMed=9748280;
RA Wang J., Ducret A., Tu Y., Kozasa T., Aebersold R., Ross E.M.;
RA "RGS21, a Gz-selective RGS protein in brain. Structure, membrane
RA association, regulation by palmitoylation, and relationship
RA to a Gz GTPase-activating protein subfamily.";
RA J. Biol. Chem. 273:26014-26025(1998).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. ACTIVITY ON G(12)-ALPHA IS INHIBITED
CC BY PHOSPHORYLATION OF THE G-PROTEIN. ACTIVITY ON G(12)-ALPHA AND
CC G(11)-ALPHA-1 IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN.
CC -!- PTM: Either Cys-2 or Cys-12 or both are palmitoylated.
CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
CC similarity).
CC -!- SIMILARITY: Contains 1 RGS domain.
CC
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CC EMBL; U27768; AAC50395.1; -.
CC EMBL; AF493328; AAM12642.1; -.
CC EMBL; BC000737; AAH00737.1; -.
CC EMBL; BC051869; AAH51869.1; -.
CC PIR; S78221; S78221.
CC HSSP; P49799; IAGR.
CC Genew; HGNC:10000; RGS4.
CC MIM; 602516; -.
CC GO; GO:0005516; F:calmodulin binding; TAS.
CC GO; GO:0005096; F:GTPase activator activity; TAS.
CC GO; GO:000188; P:inactivation of MAPK; TAS.
CC GO; GO:0008277; P:regulation of G-protein coupled receptor pr. . . ; TAS.
CC InterPro; IPR000342; Regl_Gproteins.
CC Pfam; PF00615; RGS; 1.
CC PRINTS; PR01301; RGSPTROTIN.
CC ProDom; PD001580; Regl_Gproteins; 1.
CC SMART; SM00315; RGS; 1.
CC PROSITE; PS0132; RGS; 1.
CC Signal transduction inhibitor; Lipoprotein; Palmitate;
CC phosphorylation.
CC DOMAIN 62 178 RGS.
CC LIPID 2 2 S-palmitoyl cysteine (Probable).
CC LIPID 12 12 S-palmitoyl cysteine (Probable).
CC LIPID 95 95 S-palmitoyl cysteine.

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SQ SEQUENCE 205 AA; 23255 MW; 7713F1F7496A98B CRC64;
Query Match 32.7%; Score 397.5; DB 1; Length 205;
Best Local Similarity 47.0%; Pred. No. 3.5e-23;
Matches 77; Conservative 35; Mismatches 49; Indels 3; Gaps 2;

QY 41 AKEKNRLSLLQLRPPF--HGTOASRSALLAKETRVSPBEAVKWAESFDKLLSHRDGVD 98
DB 16 AKDMKRLGLFLQKSDCHNSHNKKDKVTCQ-RVSEQEVKWAESLENLISHECGLA 74
QY 99 ATRFLKTEPSEENIEFWACEDPKCKEPOQIILKAKIYKFTQNDAPKEVNIDFHTK 158
DB 75 AFKAFKLSYSEENIDFWISCEEYKIKSPKAKIYNFISVQATKEVNLDSCTR 134

QY 159 EVIAKSIAPTLHSFDTAQSRVQLMEHDSYKRFKSETYLHLI 202
DB 135 EETSRNMLQPTTCFDEAQKIFNLMKDSYRFLKSRFYLDLV 178

RESULT 12
RGS4_MOUSE STANDARD; PRT; 205 AA.
AC O08899; Q99L30;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Regulator of G-protein signaling 4 (RGS4).
GN RGS4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Substantia nigra;
RX MEDLINE=98086343; PubMed=9425263;
RA Nomoto S., Adachi K., Yang L.X., Hirata Y., Muraguchi S., Kiuchi K.;
RT "Distribution of RGS4 mRNA in mouse brain shown by in situ
RT hybridization.";
RL Biochem. Biophys. Res. Commun. 241:281-287(1997).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
CC ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
CC THEIR INACTIVE GDP-BOUND FORM. ACTIVITY ON G(Z)-ALPHA IS INHIBITED
CC BY PHOSPHORYLATION OF THE G-PROTEIN. ACTIVITY ON G(Z)-ALPHA AND
CC G(I)-ALPHA-1 IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN (BY
CC SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN, MODERATELY
CC LOW LEVELS IN HEART, AND VERY LOW LEVELS IN LUNG, LIVER, AND
CC SKELETAL MUSCLE.

CC SEQUENCE 205 AA; 23288 MW; 5D79581711A1F67C CRC64;
Query Match 32.7%; Score 397.5; DB 1; Length 205;
Best Local Similarity 47.2%; Pred. No. 3.5e-23;
Matches 77; Conservative 34; Mismatches 49; Indels 3; Gaps 2;

QY 41 AKEKNRLSLLQLRPPF--HGTOASRSALLAKETRVSPBEAVKWAESFDKLLSHRDGVD 98
DB 16 AKDMKRLGLFLQKSDCHNSHNKKDKVTCQ-RVSEQEVKWAESLENLISHECGLA 74
QY 99 ATRFLKTEPSEENIEFWACEDPKCKEPOQIILKAKIYKFTQNDAPKEVNIDFHTK 158
DB 75 AFKAFKLSYSEENIDFWISCEEYKIKSPKAKIYNFISVQATKEVNLDSCTR 134
QY 159 EVIAKSIAPTLHSFDTAQSRVQLMEHDSYKRFKSETYLHL 201
DB 135 EETSRNMLQPTTCFDEAQKIFNLMERDSYRFLKSRFYLDL 177

RESULT 13
RGS3_MOUSE STANDARD; PRT; 568 AA.
AC Q9DC04; Q9JL22; Q9JL23;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Regulator of G-protein signaling 3 (RGS3).
GN RGS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,
RA Schriani L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Beffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=FVB/N; TISSUE=Mammary Gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Zerkow B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.O.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=20243574; PubMed=10779778;
RA Reif K., Cyster J.G.;
RT "RGS molecule expression in murine B lymphocytes and ability to
RL J. Immunol. 164:4720-4729(2000).
CC -!- FUNCTION: Inhibits signal transduction by increasing the GTPase
CC activity of G protein alpha subunits thereby driving them into
CC their inactive GDP-bound form.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q9PC04-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q9PC04-2; Sequence=VSP_005663; VSP_005664;
CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
CC similarity).
CC -!- SIMILARITY: Contains 1 RGS domain.
CC -----
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CC -----
CC EMBL: AK004648; BA523439.1; -
CC ENBL: BC033449; RAH33449.1; -
CC ENBL: AP215670; AAF34627.1; -
CC ENBL: AF215669; AAF34626.1; -
CC HSSP: P49799; 1AGR.
CC MGD: MGI:1354734; Rgs3.

DR GO: 0005634; C.nucleus; IDA.
DR InterPro: IPR000342; Regl_Gprotein.
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PRO1301; RGS-PROTEIN.
DR PRODOM: PD001580; Regl_Gprotein; 1.
DR SMART: SM00315; RGS; 1.
DR PROSITE: PS00132; RGS; 1.
KW Signal transduction inhibitor; Alternative splicing; Phosphorylation.
FT DOMAIN 443 559 Missing (in isoform Short).
FT VARSPPLIC 1 375 /FTID=VSP_005663.
FT VARSPPLIC 376 397 KMSGTDLTCEDEASRKRKKNKNI -> MLRGMVLTNRGNLQR
FT RHTMKE (in isoform Short).
FT /FTID=VSP_005664.
SQ SEQUENCE 568 AA; 61558 MW; 91939E22F3DA9F5C CRC64;
Query Match 32.6%; Score 396; DB 1; Length 568;
Best Local Similarity 44.2%; Pred. No. 1.5e-22;
Matches 80; Conservative 38; Mismatches 61; Indels 2; Gaps 1;
QY 31 EETSIEAKIR--AKEKNRLSLILQRPDPHGETQASRSALLAKETRVSPDEAVKWAESFD 88
DB 386 DEASRKRKSNIAKDMKNKLAIFRRNESPGAQPAKTKTWTXSFPTSEALKWSESLE 445
QY 89 KLLSHRDGVDATFRFLKTEPSEENIEFWACEDFKKCKPQQIILKAKAIYEKFIONDAP 148
DB 446 KLLHLKYLEVFOAFLRTEPSEENIEFWACEDFKKVKQSQAQAKKIFAEFFIAIQAC 505
QY 149 KEVNIDPHTKEVIAKTAQPTLHSEFDTAQSRYVQLMEHDSYKFLKSEYVHLIEGRPQR 208
DB 506 KEVNLDSTYREHTKENLQSIITRGCFDLAKRIEFLMEKOSYPRFLKSLDYLDLINOCKMS 565
QY 209 P 209
DB 566 P 566
RESULT 14
RGS4 RAT STANDARD; PRT; 205 AA.
AC P49799;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Regulator of G-protein signaling 4 (RGS4) (RGP4).
GN RGS4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96178495; PubMed=8602223;
RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
RT "Inhibition of G-protein-mediated MAP kinase activation by a new
RL mammalian gene family."
RL Nature 379:742-746(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Zhou M.-Y., Gomez-Sanchez C.E., Gomez-Sanchez E.P.;
RT "The complete cDNA sequence analysis of the rat RGS4."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 93-159 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96140645; PubMed=8548815;
RA Koelle M.R., Horvitz H.R.;
RT "EGL-10 regulates G protein signaling in the C. elegans nervous
RL system and shares a conserved domain with many mammalian proteins."
RL Cell 84:115-125(1996).
RN [4]
RP PHOSPHORYLATION.

RX MEDLINE=20167219; PubMed=10702309;
 RA Pedram A., Razandi M., Kehrl J., Levin E.R.;
 RT "Natriuretic peptides inhibit G protein activation. Mediation through
 cross-talk between cyclic GMP-dependent protein kinase and regulators
 of G protein-signaling proteins";
 RT J. Biol. Chem. 275:7365-7372(2000).
 RL [5]
 RN INHIBITION.
 RP MEDLINE=98016286; PubMed=9353196;
 RA Tu Y., Wang J., Ross E.M.;
 RT "Inhibition of brain Gs Gap and other RGS proteins by palmitoylation
 of G protein alpha subunits";
 RL Science 278:1132-1135(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH G(I)-ALPHA.
 RX MEDLINE=97262066; PubMed=9108480;
 RA Tesmer J.G.G., Berman D.M., Gilman A.G., Sprang S.R.;
 RT "Structure of RGS4 bound to Alpa4-activated G(i) alphas";
 RT stabilization of the transition state for GTP hydrolysis";
 RL Cell 89:251-261(1997).
 CC -!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
 ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
 THEIR INACTIVE GTP-BOUND FORM. ACTIVITY ON G(2)-ALPHA IS INHIBITED
 BY PHOSPHORYLATION OF THE G-PROTEIN. ACTIVITY ON G(2)-ALPHA AND
 G(I)-ALPHA-1 IS INHIBITED BY PALMITOYLATION OF THE G-PROTEIN.
 CC -!- PTM: Either Cys-2 or Cys-12 or both are palmitoylated (By
 similarity).
 CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase.
 CC -!- SIMILARITY: Contains 1 RGS domain.
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 or send an email to license@isb-sib.ch).
 DR EMBL; U27767; AAC52440.1; -;
 DR EMBL; AF117211; AAC12065.1; -;
 DR EMBL; U32327; AAC52367.1; -;
 DR PDB; IAGR; 16-JUN-97.
 DR PDB; IEZT; 15-JAN-01.
 DR PDB; IEZY; 15-JAN-01.
 DR InterPro: IPR000342; Regl_Gproteins.
 DR Pfam: PF00615; RGS; 1.
 DR PRINTS; PR01301; RGS-PROTEIN.
 DR ProDom; PD001580; Regl_Gproteins; 1.
 DR SMART; SM00315; RGS; 1.
 DR PROSITE; PS01132; RGS; 1.
 KW Signal transduction inhibitor; Lipoprotein; Palmitate;
 KW Phosphorylation; 3D-structure.
 RP DOMAIN 62 178 RGS
 FT LIPID 2 2 S-palmitoyl cysteine (By similarity).
 FT LIPID 12 12 S-palmitoyl cysteine (By similarity).
 FT LIPID 95 95 S-palmitoyl cysteine (By similarity).
 FT HELIX 53 59
 FT TURN 60 61
 FT HELIX 63 68
 FT HELIX 70 82
 FT TURN 83 84
 FT TURN 86 86
 FT HELIX 87 100
 FT TURN 104 106
 FT HELIX 107 118
 FT TURN 119 119
 FT TURN 121 122
 FT TURN 124 125
 FT HELIX 131 140
 FT TURN 141 142
 FT TURN 146 149
 FT TURN 150 162
 FT HELIX 163 163
 FT TURN

FT HELIX 164 168
 FT TURN 169 170
 FT HELIX 172 175
 FT TURN 176 176
 SQ SEQUENCE 205 AA; 23248 MW; 9647C0EC909D0F6F CRC64;
 Query Match 32.6%; Score 395.5; DB 1; Length 205;
 Best Local Similarity 46.6%; Pred. No. 4.9e-23;
 Matches 76; Conservative 36; Mismatches 48; Indels 3; Gaps 2;
 QY 41 AKERNRLSLLQRPDF--HGCTOASRSALLAKETRVSPPEAVKWAESFDKLLSHRDQVD 98
 DQ 16 AKDMKRLGLFLQKSDCEHSSSHSKDKVTCQ-RVSEQEVKWAESLENLNHCEGLA 74
 QY 99 APTFLTKTEFSEENIEFWACEDPKCKEFCQQLIKAKAIYKFIQNDAPKVNIDFHTK 158
 DQ 75 AFKAPLXSEYSEENIDFWISCEYKIKSPKSLPKAKIYNEFISVQATKEVNLDSCTR 134
 QY 159 EVIAKSIQAPTLHSFDTAQSRVYQLMEHDSYKRFKSETVYHL 201
 DQ 135 EETSRNMLEPITTCFDEAQKKIFNLMEKDSYRRFLKSRFYLDL 177
 RESULT 15
 RGS3 HUMAN STANDARD; PRT; 51.9 AA.
 ID P49736, Q8TD59; Q8TD68;
 AC 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)
 DE Regulator of G-protein signaling 3 (RGS3) (RGP3).
 GN RGS3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=96178495; PubMed=8602223;
 RA Druey K.M., Blumer K.J., Kang V.H., Kehrl J.H.;
 RT "Inhibition of G-protein-mediated MAP kinase activation by a new
 mammalian gene family";
 RL Nature 379:742-746(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RA Publ H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Skuce C.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Inhibits signal transduction by increasing the GTPase
 activity of G protein alpha subunits thereby driving them into
 their inactive GDP-bound form.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P49796-1; Sequence=Displayed;
 CC Name=2; Synonyms=RGS3T;
 CC IsoId=P49796-2; Sequence=VSP_005662;
 CC -!- PTM: Phosphorylated by cyclic GMP-dependent protein kinase (By
 similarity).
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).

```

CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U27655; AAC50394.1; -.
DR EMBL; AF493927; AM12641.1; -.
DR EMBL; AF493941; AM12655.1; -.
DR EMBL; AL162727; CAC78977.1; -.
DR PIR; S78089; S78089.
DR HSSP; P49799; IAGR.
DR Genew; HGNC:9999; RGS3.
DR MIM; 602189; -.
DR GO; GO:0005829; Cytosol; TAS.
DR GO; GO:0005096; F:GTPase activator activity; TAS.
DR GO; GO:000188; P:inactivation of MAPK; TAS.
DR GO; GO:0008277; P:regulation of G-protein coupled receptor pr. .; TAS.
DR InterPro; IPR000342; Regl_Gprotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50132; RGS; 1.
KW Signal transduction inhibitor; Alternative splicing; Phosphorylation.
FT DOMAIN 394 510
FT VARSPLIC 1 313 Missing (in isoform 2).
FT CONFLICT 305 305 K -> R (IN REF. 2).
FT SEQUENCE 519 AA; 56601 MW; F1CFE3F27D4673A0 CRC64;

Query Match 31.5%; Score 383; DB 1; Length 519;
Best Local Similarity 43.7%; Pred. No. 1.3e-21;
Matches 76; Conservative 35; Mismatches 63; Indels 0; Gaps 0;

QY 36 EAKIRAKERNRLSLLQRPDFHGETQASRSALLAKETRVSPPEAVKWAESFDKLLSHRD 95
Db 344 KSKNLAKDMKNKLGIPRRNESPGAPPAGKADMMKSPKPTSEALKWGESLEKLLVHKY 403

QY 96 GVDAPTRFLKTEFSEENIEFWACEDFKCKBPQQIILKAKAIYEKFIQNDAPKEVNIDF 155
Db 404 GLAVFQAFRLTEFSEENLEFWLACEDFKKVSQSKVASKAKIFAEYIAIQACKEVNLD 463

QY 156 HTKEVIAKSTAOPLHSFDTAQSRVYQLMEHDSYKFLKSETYHLIEGRPQP 209
Db 464 YTREHTKDNLQSVTRCGCFDLAQRIEGLMEKDSYPRFLRSDLYLDLINQKXSP 517

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Search completed: August 20, 2004, 16:41:30
Job time : 15.5 secs

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OM protein - protein search, using sw model

Run on: August 20, 2004, 15:52:01 ; Search time 74.5 Seconds

(without alignments)
995.259 Million cell updates/sec

Title: US-09-894-749-4
Perfect score: 1214
Sequence: 1 MDSLVSFFSQLNMCSEKKT.....SRSTFYNDQDVKSDVAIWL 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	421	34.7	213	13 Q7ZZS4	Q7ZZS4 gallus gall
2	421	34.7	225	13 Q7ZZS5	Q7ZZS5 gallus gall
3	411.5	33.9	164	6 Q8XV9	Q8XV9 ovis aries
4	410.5	33.8	180	11 Q8BXT1	Q8BXT1 mus musculus
5	406.5	33.5	181	6 Q8E4Z2	Q8E4Z2 sus scrofa
6	404.5	33.3	196	6 Q9SK68	Q9SK68 macaca fasc
7	404	33.3	208	13 Q7SZC6	Q7SZC6 gallus gall
8	400.5	33.0	182	13 Q7R2D3	Q7R2D3 brachydanio
9	397	32.7	283	13 Q7SYI2	Q7SYI2 gallus gall
10	397	32.7	408	13 Q7SYI1	Q7SYI1 gallus gall
11	397	32.7	441	13 Q7SYI0	Q7SYI0 gallus gall
12	387	32.7	799	13 Q7SYH9	Q7SYH9 gallus gall
13	386	32.6	930	11 Q9Z5G9	Q9Z5G9 mus musculus
14	381	32.2	967	11 Q9Z0Q9	Q9Z0Q9 rattus norv
15	384	31.6	319	4 Q8NFN6	Q8NFN6 homo sapien
16	383	31.5	917	4 Q8NFN4	Q8NFN4 homo sapien

17	383	31.5	917	4 Q8WXA0	Q8WXA0 homo sapien
18	383	31.5	917	4 Q8IUQ1	Q8IUQ1 homo sapien
19	383	31.5	1093	4 Q8NFN5	Q8NFN5 homo sapien
20	382	31.5	192	4 Q8WVE9	Q8WVE9 homo sapien
21	381	31.4	192	4 Q8WV02	Q8WV02 homo sapien
22	380	31.3	284	4 Q96NV5	Q96NV5 homo sapien
23	377	31.1	168	13 Q7SVI3	Q7SVI3 gallus gall
24	356	29.3	235	11 Q80V16	Q80V16 mus musculus
25	355.5	29.3	204	13 Q919D9	Q919D9 xenopus lae
26	352.5	29.0	201	11 Q7INU9	Q7INU9 mus musculus
27	309	25.5	271	5 Q9V888	Q9V888 drosophila
28	309	25.5	274	5 Q8T017	Q8T017 drosophila
29	306.5	25.2	194	11 Q8BFU4	Q8BFU4 mus musculus
30	304	25.0	158	11 Q8K443	Q8K443 mus musculus
31	303.5	25.0	194	11 Q8CGT5	Q8CGT5 mus musculus
32	301.5	24.8	220	13 Q7T0Q6	Q7T0Q6 xenopus lae
33	300.5	24.8	220	13 Q8QHK0	Q8QHK0 xenopus lae
34	300	24.7	208	11 Q8CSJ7	Q8CSJ7 mus musculus
35	297.5	24.5	199	13 Q8AYF2	Q8AYF2 gallus gall
36	297	24.5	210	11 Q8CSF3	Q8CSF3 mus musculus
37	296	24.4	230	11 Q8BR34	Q8BR34 mus musculus
38	294	24.2	150	4 Q8T061	Q8T061 homo sapien
39	291.5	24.0	181	5 Q9TVK0	Q9TVK0 caenorhabdi
40	290	23.9	244	5 Q96842	Q96842 drosophila
41	280.5	23.1	181	4 Q96GNO	Q96GNO homo sapien
42	273.5	22.5	424	5 Q95Q48	Q95Q48 caenorhabdi
43	273.5	22.5	475	4 Q7Z4K3	Q7Z4K3 homo sapien
44	273.5	22.5	477	4 Q7Z4K4	Q7Z4K4 homo sapien
45	273.5	22.5	480	4 Q7Z4K5	Q7Z4K5 homo sapien

ALIGNMENTS

RESULT 1

Q7ZZS4 PRELIMINARY; PRT; 213 AA.
ID Q7ZZS4
AC Q7ZZS4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Regulator of G-protein signaling protein 2.
GN RGS2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tosetti P., Parente V., Taglietti V., Dunlap K., Toselli M.;
RT "Concentration-dependent effects of chick RGS2L on neuronal L-type Ca channel modulation by bradykinin.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF502149; AAP30802.1; .
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPR000342; Regl_Gpotein.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gpotein; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS00132; RGS; 1.
SQ SEQUENCE 213 AA; 24786 MW; BOCAD39ACC496D1E CRC64;

Query Match 34.7%; Score 421; DB 13; Length 213;
Best Local Similarity 50.3%; Pred.No.1.4e-25;
Matches 83; Conservative 31; Mismatches 51; Indels 0; Gaps 0;
Qy 42 KEKENLSLLIQRDFHGETQASRSALLAKETRVSPSEAVKWAESFFKLISHRDGVDAFT 101
Db 41 KDWKLLSYFLQNSRSRSKVRKAGKHHTYFRSPPEARLWSAFDELLANKYGVAAFR 100
Qy 102 RLKTEFSEENIEFWVACEDFKCKEFPQIILKAKAIYFKFIQNDAPKEVNIDFHTKEVI 161

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Db 101 AFLKSEFCENIEFWLACEDFKTKSPQKLTAKKAIYNDIEFKAPKEINIDFQTKNMI 160
QY 162 AKSIAPOTLHSDPTAQSRVYQVLMHDSYKRFKSEYLYHLIEGRP 206
Db 161 AQNLQBATHTCSAAQKRVYSLMNNNSYPRFLESFYQELCKKPP 205

RESULT 2
Q72ZS5 PRELIMINARY; PRT; 225 AA.
AC Q72ZS5;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Regulator of G-protein signaling protein 2 long isoform.
GN RGS2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tosetti P., Parente V., Taglietti V., Dunlap K., Toselli M.;
RT "Concentration-dependent effects of chick RGS2L on neuronal L-type Ca
RT channel modulation by bradykinin."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF502148; AAP30801.1; -
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPRO00342; Regl_Gproteins.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50132; RGS; 1.
SQ SEQUENCE 225 AA; 25956 MW; 5F8C5FAE2C665EE1 CRC64;

Query Match 34.7%; Score 421; DB 13; Length 225;
Best Local Similarity 50.3%; Pred. No. 1.5e-25;
Matches 83; Conservative 31; Mismatches 51; Indels 0; Gaps 0;

QY 42 KEKRNLSLLQRPDPFHGETQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFT 101
Db 53 KQWKKSLYFLQNSRSSKVKSTKAGKHHTYRPSPEARLWSEAFDELLANKYGVAAFR 112
QY 102 RFLKTSFENIEFWVACEDFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNDIHTKEVI 161
Db 113 AFLKSEFCENIEFWLACEDFKTKSPQKLTAKKAIYNDIEFKAPKEINIDFQTKNMI 172
QY 162 AKSIAPOTLHSDPTAQSRVYQVLMHDSYKRFKSEYLYHLIEGRP 206
Db 173 AQNLQBATHTCSAAQKRVYSLMNNNSYPRFLESFYQELCKKPP 217

RESULT 3
Q8HXV9 PRELIMINARY; PRT; 164 AA.
AC Q8HXV9;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE RGS2 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Nlend M.C., Bookman R.J., Conner G.E., Salathe M.;
RC TISSUE=Airway;
RA Nlend M.C., Bookman R.J., Conner G.E., Salathe M.;
RT "RGS2 Modulates Purinergic Calcium and Ciliary Beat Frequency

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RT Responses in Airway Epithelia."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF472577; AAN32893.1; -
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPRO00342; Regl_Gproteins.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50132; RGS; 1.
DR NON_TER 1
FT NON_TER 164
SQ SEQUENCE 164 AA; 18947 MW; EB5B828CB05E43D5 CRC64;

Query Match 33.9%; Score 411.5; DB 6; Length 164;
Best Local Similarity 51.2%; Pred. No. 5.8e-25;
Matches 84; Conservative 28; Mismatches 51; Indels 1; Gaps 1;

QY 47 RLSLLQRPDPFHGETQASRSALLAKETRVSPPEAVKWAESFDKLLSHRDGVDAFTFLKT 106
Db 2 RLSYFLQNSSPGPKPTGKKSKQOTFIKPSPEAQWSEAFDELLASKYGLAAFRFLKS 61
QY 107 EFGSENIIEFWVACEDFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNDIHTKEVIKASIA 166
Db 62 EYCEENIEFWLACEDFKTKSPQKLTAKKAIYNDIEFKAPKEINIDFQTKLIAQNIQ 121
QY 167 OPTLHSDPTAQSRVYQVLMHDSYKRFKSEYLYHLIEGRP 210
Db 122 EATSGCFTTAQKRVYSLMNNNSYPRFLESFYQDLCQ-RPQITT 164

RESULT 4
Q8BXT1 PRELIMINARY; PRT; 180 AA.
AC Q8BXT1;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Regulator of G-protein signaling 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RA MEDLINE=22354683; PubMed=124566851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK044337; BAC31874.1; -
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR InterPro; IPRO00342; Regl_Gproteins.
DR Pfam; PF00615; RGS; 1.
DR PRINTS; PR01301; RGS-PROTEIN.
DR ProDom; PD001580; Regl_Gproteins; 1.
DR SMART; SM00315; RGS; 1.
DR PROSITE; PS50132; RGS; 1.
SQ SEQUENCE 180 AA; 20963 MW; 00FC35B572785856 CRC64;

Query Match 33.8%; Score 410.5; DB 11; Length 180;
Best Local Similarity 48.3%; Pred. No. 7.8e-25;
Matches 84; Conservative 31; Mismatches 50; Indels 9; Gaps 2;

QY 40 RAXEKNRSLILLQRPDPFHGETQASRSALLAKES-----TRVSPPEAVKWAESFDKLLSHR 94
Db 9 RNKGMTRLCCLSHKSD-----SCSDFTAILDPKPNALKRLSTEEATRWAESEFDVLLSHK 64
QY 95 DGVDAFTFLKTEFSEENIEFWVACEDFKKCKEPOQIILKAKAIYEKFIQNDAPKEVNDI 154
Db 65 YGVAAPFAFLKTEFSEENIEFWLACEDFKTKRSTAKLVTKAHRIFEFVDVQAPREVNDI 124

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RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RGS DOMAIN.
DR EMBL: BAB62198.1; -.
DR GO: GO:0004871; F:signal transducer activity; IEA.
DR InterPro: IPR000342; Regl_Gpotein.
DR Pfam: PF00615; RGS; 1.
DR PRINTS: PR01301; RGS-PROTEIN.
DR ProDom: PD001580; Regl_Gpotein; 1.
DR SMART: SM00315; RGS; 1.
DR PROSITE: PS00132; RGS; 1.
DR Hypothetical protein.
SQ SEQUENCE 196 AA; A42C6D41A9244064 CRC64;

Query Match 33.3%; Score 404.5; DB 6; Length 196;
Best Local Similarity 45.7%; Pred. No. 2.6e-24;
Matches 85; Conservative 29; Mismatches 55; Indels 17; Gaps 2;

QY 40 RAKEKNRLSLLQRPDFHGETQA-----SRSAI-----LAKETRVSPPEAVK 82
DB 9 RNKGMRTRLGCLSHKSDSCSDFTAILPDKPNRALNYLRMYKFTATELQESRRLSTEBATR 68

QY 83 WARESPKLLSHRPGVDVAFTRFLKTEFSEENIEFWACEDFKCKEPOQIILKAKAIYEKF 142
DB 69 WADSFVLLSHKYGVAAFRAFLKTEFSEENLEFWLACEEFKKTAKLISKAHRIPEEF 128

QY 143 IQNDAPKEVNIDFHTKEVIAKSIQAQPLTHSDFTAQSRVYQLMHDSYKRFKLSYTLHLI 202
DB 129 VDVQAPREVNIDFQTRATKNQWESLTCFDQAQGVKHSIMEKDSYRFLRSKMYLDLL 188

QY 203 EGRPQR 208
DB 189 SOSQRR 194

RESULT 7
Q7SZC6 PRELIMINARY; PRT; 208 AA.
AC Q7SZC6
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Regulator of G-protein signaling 4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=D4 hindbrain;
RA Grillet N., Dubreuil V., Dufour H., Goridis C., Brunet J.-F.;
RT "Dynamic expression of RGS4 in the developing nervous system and
RT control by the paired-like homeoprotein Phox2b."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY297457; AAP57222.1; -.
DR SEQUENCE 208 AA; 23523 MW; 838B31750F0EA68 CRC64;

Query Match 33.3%; Score 404; DB 13; Length 208;
Best Local Similarity 47.2%; Pred. No. 3e-24;
Matches 85; Conservative 35; Mismatches 50; Indels 10; Gaps 5;

QY 41 AKERNRLSLLIQRPDF--HGTEQSRSAALLAKETRVSPPEAVKWAESFDKLLSHRGVD 98
DB 16 AKDMKRLGVLLQKSDSCDGGSGGKKERVSSQ-RVSGBEVKKWAESLENLIHHRGLA 74

QY 99 AFRFLKTEFSEENIEFWACEDFKCKEPOQIILKAKAIYEKFIQNDAPKEVNIDFHTK 158
DB 75 AFRAFLKSEYSEENIEFWWSSCEDYKKTSPAKLSTARKIYDEFISVQATKEVNLDSCTR 134

QY 159 EVTKAGIAQPLTHSPFTAQSRVQLMHDSYKRFKLSYTLHLIEGRPQ-----PTNLRR 214
DB 135 EKTSHNMLEPTLSCFDEAQRKIFLMEKDSYRRFLKS--PYLDLVS--PPRAGCGPENCKR 191

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RESULT 8
Q7T2D3 PRELIMINARY; PRT; 182 AA.
AC Q7T2D3;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054594; AAHS4594.1; -.
KW Hypothetical protein.
SQ SEQUENCE 182 AA; 21053 MW; 4D502817AA8CB4FF CRC64;

Query Match 33.0%; Score 400.5; DB 13; Length 182;
Best Local Similarity 47.5%; Pred. No. 4.9e-24;
Matches 85; Conservative 29; Mismatches 52; Indels 13; Gaps 3;

QY 32 ETSIEAKIR--AKEKNRNLSSLLQRPDPFHGETQASRSALLAKETRVSPPEAVKWA 84
Db 10 QICLE---RAKEIKTKLGLLQKPNISIDLIIPYQEKPEKKLQKAT---PEEAQWR 63
QY 85 ESDKLLSHRDGVDAFTRLKTEFSEENIEFWACEDFKCKEPOQIILKAKIYEKIQ 144
Db 64 ESLDKVLSNYSGLATFKSLRSEFSEENIEFWACEDFKKTKNPKMKATKAKKIYEDFIQ 123
QY 145 NDAPKEVNTDFHTKEVIAKSIQPTLHSDFTAQSRVYQLMHDSYKRFKSEYTLHLIE 203
Db 124 TCGPKEVNIIDHFKVDVTLNLDVLSSTFELAQSRITLMEKDSGFRFLRSQYQELK 182

RESULT 9
Q7SYI2 PRELIMINARY; PRT; 283 AA.
AC Q7SYI2;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN SEQUENCE FROM N.A.
RP TISSUE=DRG neuron;
RC MEDLINE=22694492; PubMed=12771384;
RA Tosetti P., Pathak N., Jacob M.H., Dunlap K.;
RT "RGS3 mediates a calcium-dependent termination of G protein signaling
RT in sensory neurons."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7337-7342 (2003).
DR EMBL; AY124775; AAM94021.1; -.
SQ SEQUENCE 408 AA; 45438 MW; 75B50794F22E74B5 CRC64;

Query Match 32.7%; Score 397; DB 13; Length 408;
Best Local Similarity 45.4%; Pred. No. 2.4e-23;
Matches 79; Conservative 38; Mismatches 55; Indels 2; Gaps 1;

QY 31 ETSIEAKIR--AKEKNRNLSSLLQRPDPFHGETQASRSALLAKETRVSPPEAVKWAESFD 88
Db 226 EETSRRKRSLSLAKDMKNRLGIFRRNESPGANPSSKLDKVLKSLKPAPEALKWGESLE 285
QY 89 KLLSHRDGVDAFTRLKTEFSEENIEFWACEDFKCKEPOQIILKAKIYEKIQNDAP 148
Db 286 KLLHLKYGLAAFRFLRTFSEENIEFWACEDFKCKEPOQIILKAKIYEKIQNDAP 345
QY 149 KEVNDPHTKEVIAKSIQPTLHSDFTAQSRVYQLMHDSYKRFKSEYTLHLI 202
Db 346 KEVNDLSYTRHTYKENLQNTRCFDLAQKRIYGLMEKDSYFPFLRSDLVDII 399

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RP TISSUE=DRG neuron;
RC MEDLINE=22694492; PubMed=12771384;
RA Tosetti P., Pathak N., Jacob M.H., Dunlap K.;
RT "RGS3 mediates a calcium-dependent termination of G protein signaling
RT in sensory neurons."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7337-7342 (2003).
DR EMBL; AY124774; AAM94020.1; -.
SQ SEQUENCE 283 AA; 32070 MW; 5C9871357F00A195 CRC64;

Query Match 32.7%; Score 397; DB 13; Length 283;
Best Local Similarity 45.4%; Pred. No. 1.5e-23;
Matches 79; Conservative 38; Mismatches 55; Indels 2; Gaps 1;

QY 31 ETSIEAKIR--AKEKNRNLSSLLQRPDPFHGETQASRSALLAKETRVSPPEAVKWAESFD 88
Db 101 EETSRRKRSLSLAKDMKNRLGIFRRNESPGANPSSKLDKVLKSLKPAPEALKWGESLE 160
QY 89 KLLSHRDGVDAFTRLKTEFSEENIEFWACEDFKCKEPOQIILKAKIYEKIQNDAP 148
Db 161 KLLHLKYGLAAFRFLRTFSEENIEFWACEDFKCKEPOQIILKAKIYEKIQNDAP 220
QY 149 KEVNDPHTKEVIAKSIQPTLHSDFTAQSRVYQLMHDSYKRFKSEYTLHLI 202
Db 221 KEVNDLSYTRHTYKENLQNTRCFDLAQKRIYGLMEKDSYFPFLRSDLVDII 274

RESULT 10
Q7SYII PRELIMINARY; PRT; 408 AA.
AC Q7SYII;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
OS Regulator of G protein signaling 3 RGS3s isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RP TISSUE=DRG neuron;
RC MEDLINE=22694492; PubMed=12771384;
RA Tosetti P., Pathak N., Jacob M.H., Dunlap K.;
RT "RGS3 mediates a calcium-dependent termination of G protein signaling
RT in sensory neurons."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7337-7342 (2003).
DR EMBL; AY124775; AAM94021.1; -.
SQ SEQUENCE 408 AA; 45438 MW; 75B50794F22E74B5 CRC64;

Query Match 32.7%; Score 397; DB 13; Length 408;
Best Local Similarity 45.4%; Pred. No. 2.4e-23;
Matches 79; Conservative 38; Mismatches 55; Indels 2; Gaps 1;

QY 31 ETSIEAKIR--AKEKNRNLSSLLQRPDPFHGETQASRSALLAKETRVSPPEAVKWAESFD 88
Db 226 EETSRRKRSLSLAKDMKNRLGIFRRNESPGANPSSKLDKVLKSLKPAPEALKWGESLE 285
QY 89 KLLSHRDGVDAFTRLKTEFSEENIEFWACEDFKCKEPOQIILKAKIYEKIQNDAP 148
Db 286 KLLHLKYGLAAFRFLRTFSEENIEFWACEDFKCKEPOQIILKAKIYEKIQNDAP 345
QY 149 KEVNDPHTKEVIAKSIQPTLHSDFTAQSRVYQLMHDSYKRFKSEYTLHLI 202
Db 346 KEVNDLSYTRHTYKENLQNTRCFDLAQKRIYGLMEKDSYFPFLRSDLVDII 399

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RESULT 11

ID Q7SY10 PRELIMINARY; PRT; 441 AA.

AC Q7SY10; 25, Created

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Regulator of G protein signaling 3 (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=DRG neuron;

RC MEDLINE=22684492; PubMed=12771384;

RC Tosetti P., Pathak N., Jacob M.H., Dunlap K.;

RT "RGS3 mediates a calcium-dependent termination of G protein signaling

RT in sensory neurons."

RL Proc. Natl. Acad. Sci. U.S.A. 100:7337-7342(2003).

DR EMBL, AY124776; AAM94022.1; --.

DR NON_TER

DR SEQUENCE 441 AA; 48612 MW; F5B92C9C25EB70F CRC64;

FT SQ

Query Match 32.7%; Score 397; DB 13; Length 441;

Best Local Similarity 45.4%; Pred. No. 2,6e-23;

Matches 79; Conservative 38; Mismatches 55; Indels 2; Gaps 1;

QY 31 ETSIEAKTR--AKEKRNLSLLQRPDPFHGTQASRSALLAKETRVSPPEAVKWSFD 88

DB 259 EETSRKGRSLAKDMKNLGIFFRRNESPANGPSSKLDKVLKSLKPAPEALKWGESLE 318

QY 89 KULSHRDGVDAFTRFLKTEFSEENIEFWVACEDFKKCKEPOQILKAKAIYEKFIQNDAP 148

DB 319 KULLHKYGLAFAFLRTEFSEENIEFWVACEDFKKCKEPOQILKAKAIYEKFIQNDAP 378

QY 149 KEVNIDFHTKEVIAKSIAQPTLHSPDTAQSRVYQVLMEDHSYKRFKSKETYLHLI 202

DB 379 KEVNLDSTYREHTKENLQITRGCFDLAQKRIYGLMKDYSYPRFLRSYLDLII 432

RESULT 12

ID Q7SYH9 PRELIMINARY; PRT; 799 AA.

AC Q7SYH9; 25, Created

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Regulator of G protein signaling 3 RGS3L isoform.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=DRG neuron;

RC MEDLINE=22684492; PubMed=12771384;

RC Tosetti P., Pathak N., Jacob M.H., Dunlap K.;

RT "RGS3 mediates a calcium-dependent termination of G protein signaling

RT in sensory neurons."

RL Proc. Natl. Acad. Sci. U.S.A. 100:7337-7342(2003).

DR EMBL, AY124777; AAM94023.1; --.

DR SEQUENCE 799 AA; 89511 MW; D0A818CF0B282B2A CRC64;

FT SQ

Query Match 32.7%; Score 397; DB 13; Length 799;

Best Local Similarity 45.4%; Pred. No. 5,3e-23;

Matches 79; Conservative 38; Mismatches 55; Indels 2; Gaps 1;

QY 31 ETSIEAKTR--AKEKRNLSLLQRPDPFHGTQASRSALLAKETRVSPPEAVKWSFD 88

DB 617 EETSRKGRSLAKDMKNLGIFFRRNESPANGPSSKLDKVLKSLKPAPEALKWGESLE 676

RESULT 13

ID Q925G9 PRELIMINARY; PRT; 930 AA.

AC Q925G9; 19, Created

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE PDZ-RGS3 protein.

GN RGS3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21197945; PubMed=11301003;

RC Lu Q., Sun E.E., Klein R.S., Flanagan J.G.;

RT "Ephrin-b reverse signaling is mediated by a novel PDZ-RGS protein and

RT selectively inhibits G protein-coupled chemoattraction."

RL Cell 105:69-79(2001).

CC -|- SIMILARITY: CONTAINS 1 RGS DOMAIN.

CC -|- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.

DR EMBL; AF350047; AAK38878.1; --.

DR MGD; MGI:1354734; RGS3.

DR GO; GO:0005634; C:nucleus; IDA.

DR InterPro; IPR001478; PDZ;

DR InterPro; IPR000342; Regl_Gpotein.

DR Pfam; PF00595; PDZ; 1.

DR Pfam; PF00615; RGS; 1.

DR PRINTS; PR01301; RGS-PROTEIN.

DR ProDom; PD001580; Regl_Gpotein; 1.

DR SMART; SM00228; PDZ; 1.

DR SMART; SM00315; RGS; 1.

DR PROSITE; PS50106; PDZ; 1.

DR PROSITE; PS50132; RGS; 1.

DR SEQUENCE 930 AA; 102511 MW; FB0ECEA164D2F6A1 CRC64;

FT SQ

Query Match 32.6%; Score 396; DB 11; Length 930;

Best Local Similarity 44.2%; Pred. No. 7,6e-23;

Matches 80; Conservative 38; Mismatches 61; Indels 2; Gaps 1;

QY 31 EETSIEAKTR--AKEKRNLSLLQRPDPFHGTQASRSALLAKETRVSPPEAVKWSFD 88

DB 748 DEASRRKRSKNTAKDMKNLGIFFRRNESPANGPSSKLDKVLKSLKPAPEALKWGESLE 807

QY 89 KULSHRDGVDAFTRFLKTEFSEENIEFWVACEDFKKCKEPOQILKAKAIYEKFIQNDAP 148

DB 808 KULLHKYGLAFAFLRTEFSEENIEFWVACEDFKKCKEPOQILKAKAIYEKFIQNDAP 867

QY 149 KEVNIDFHTKEVIAKSIAQPTLHSPDTAQSRVYQVLMEDHSYKRFKSKETYLHLI 208

DB 868 KEVNLDSTYREHTKENLQITRGCFDLAQKRIYGLMKDYSYPRFLRSYLDLII 927

QY 209 P 209

DB 928 P 928

RESULT 14

ID Q920Q9 PRELIMINARY; PRT; 967 AA.

AC Q920Q9; 19, Created

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

